

165565

STIC-Biotech/ChemLib

mg

From: Whiteman, Brian
Sent: Tuesday, September 13, 2005 1:42 PM
To: STIC-Biotech/ChemLib
Subject: seq search

RECEIVED
SEP 13 2005
BIOCH/CHEM DIVISION
(STIC)

09/380,203 La Monte et al. 2/26/98

search seq id no: 1 against DNA

1) the commercial databases, and the issued and published US application databases

search seq id no: 2 against dna and amino acid

1) the commercial databases, and the issued and published US application databases

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

9/13/05
1 - NA - QSH
1 - AA - QAP
1 - AA - reverse to
NA

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2005, 20:33:38 ; Search time 5428 Seconds
(without alignments)
3347.588 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MEFSLLPRLECNCAISRAH.....FIRGGVSPVLSGWSQTPDLR 375

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

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Database :

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SUMMARIES

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1	2034	100.0	1442	6	AR051550 Sequence
2	2034	100.0	1442	6	AR072690 Sequence
3	2034	100.0	1442	6	AR073235 Sequence
4	2034	100.0	1442	6	AX594290 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	2034	100.0	1442	6	AX709024	Sequence
7	2034	100.0	1442	6	AX709356	Sequence
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9	2034	100.0	1442	6	AX774635	Sequence
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11	2034	100.0	1442	9	AF010144	Homo sapi
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14	1520	74.7	1381	6	AR051479	Sequence
15	1520	74.7	1381	6	AR072619	Sequence
16	1520	74.7	1381	6	AR073164	Sequence
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20	968	47.6	220384	2	AC078926	Human sapi
21	967.5	47.6	105921	9	AC004263	Human sapi
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24	949	46.7	72826	9	AL391539	Human DNA
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ALIGNMENTS

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ACCESSION	AR051550	Sequence 120 from patent US 5830670.	1442 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR051550.1	GI:5974914	1442 bp	DNA	linear	PAT 29-SEP-1999
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1442)					
AUTHORS	de la Monte, S. and Wands, J.R.					
TITLE	Neural thread protein gene expression and detection of Alzheimer's disease					
JOURNAL	Patent: US 5830670-A 120 03-NOV-1998;					
FEATURES	Location/Qualifiers					
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	Percent Similarity:	100.00%	Mismatches:	0
	Best local Similarity:	100.00%	Indels:	0
	Query Match:	100.00%	Gaps:	0
DB:		6		

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QY	21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db	75 AACCTCCGGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCTCCCGCTCAGCTGGGATT 134
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Db	135 ACAGGCATGTGCACCGCTCGGCTAAATTTTGTATTTTATTTTATTTAGTAGAGATGGAGTTT 194
QY	61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerValSerAla 80
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QY	81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
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QY	161 HisSerSerLeuGlnProSerThrProGluIleLysHisProAlaSerAlaSerGln 180
Db	495 CACAGCTCACTGCAGCTTCAACTCTTGAGATCAAGCATCTCTCTGCTCAGCTCCCA 554
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QY	221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
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QY	301 LeuPheGluMetGlnSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
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QY	321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
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QY	341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
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LOCUS	Sequence 120 from patent US 5948634.
DEFINITION	AR072690
ACCESSION	AR072690.1 GI:9999454
VERSION	AR072690.1
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1442)
AUTHORS	de la Monte,S. and Wands,J.R.
TITLE	Neural thread protein gene expression and detection of alzheimer's disease
JOURNAL	Patent: US 5948634-A 120 07-SEP-1999;
FEATURES	Location/Qualifiers
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Pred. No.:	4,69e-142 Length: 1442
Score:	2034.00 Matches: 375
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
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QY	21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db	75 AACCTCCGGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCTCCCGCTCAGCTGGGATT 134
QY	41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db	135 ACAGGCATGTGCACCGCTCGGCTAAATTTTGTATTTTATTTTATTTAGTAGAGATGGAGTTT 194
QY	61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerValSerAla 80
Db	195 CTCCATGTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATCCCTCCGCTCGGGC 254
QY	81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db	255 TCCCAAGTGTAGATACAGGCTGGCCACCATGCGCGCTCTGCTGGCTAAATTTTGT 314
QY	101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
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QY	161 HisSerSerLeuGlnProSerThrProGluIleLysHisProAlaSerAlaSerGln 180
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QY	181 ValAlaGlyThrLysAspMetHisIstYrThrTrpLeuIlePheIlePheAsn 200
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QY	281 SerGlnSerAlaGlyIleThrGlyValSerHisAlaArgLeuIlePheAsnPheCys 300
Db	855 TCCCAAGTGTGGGATTACAGGCTGAGCCACCGCCCGCTGATCTGCTCGCTCGCGCC 914
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QY	321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
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QY	341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360

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 VERSION AR073235.1 GI:9999998
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 ORGANISM Unclassified.
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 AUTHORS de la Monte, S. and Wands, J.R.
 TITLE Neural thread protein gene expression and detection of Alzheimer's disease
 JOURNAL Patent: US 5948888-A 120 07-SEP-1999;
 FEATURES Location/Qualifiers
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 Score: 2034.00 Matches: 375
 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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RESULT 4
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AX594290.1 GI:28375449
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Averback, P.
METHODS of using neural thread proteins to treat tumors and other
conditions requiring the removal or destruction of cells
Patent: WO 02074323-A 1 26-SEP-2002;
AVERBACK, Paul (CA)
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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ORIGIN

Alignment Scores:
Pred. No.: 4,69e-142 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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AX709024 1442 bp DNA linear PAT 04-APR-2003
LOCUS Sequence 48 from Patent WO03008443.
DEFINITION AX709024
ACCESSION AX709024
VERSION AX709024.1 GI:29564697
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Averback,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 48 30-JAN-2003;
Nymox Corporation (CA)
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Alignment Scores:
Pred. No.: 4,69e-142 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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AX709356
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DEFINITION Sequence 1 from Patent WO02092115.
ACCESSION AX709356
VERSION AX709356.1 GI:29564893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
TITLE Method of preventing cell death using segments of neural thread
JOURNAL proteins
Patent: WO 02092115-A 1 21-NOV-2002;
NYMOX CORPORATION (CA)
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ACCESSION AX770807
VERSION AX770807.1 GI:32437975
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
Averback, P.A. and Gemmell, J.
Peptides effective in the treatment of tumors and other conditions
requiring the removal or destruction of cells
Patent: WO 03008444-A 125 30-JAN-2003;
NYMOX CORPORATION (CA)
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ORIGIN

Alignment Scores:

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Pred. No.: 4,69e-142 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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US-09-380-203-2 (1-375) x AX770807 (1-1442)

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Db      915  TTGTTTGAATGGAATCTCACTCTGTACCCAGGCTGAGTGCATGGCAATCGCCAAATCTCGGC 974
Qy      321  SerLeuGlnProLeuProGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 340
Db      975  TCACTGCAACCTCTGCCTCCCGGCTCAAGCGATTCTCTGCTCAGCCTCCCAAGCAGC 1034
Qy      341  TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db      1035  TGGGATTTAGGGACCTGCGCACACACCGCCGCTAATTTTTTGTATTTTCAATTAGAGCGGG 1094
Qy      361  ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db      1095  GTTTCACCATATTTGTGAGCGTGGTCTCAAACTCTGACCTCAGG 1139

RESULT 9
AX774635
LOCUS      1442 bp      DNA      linear      PAT 09-JUL-2003
DEFINITION      Sequence 53 from Patent WO02097030.
ACCESSION      AX774635
VERSION      AX774635.1 GI:32486166
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Averbach, P.A.
TITLE      Peptides derived from neural thread proteins and their medical use
JOURNAL      Patent: WO 02097030-A 53 05-DEC-2002;
NYMOX CORPORATION (CA)
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HSSLQSPPEIKHPASASQVAGTKDMHYTWLIFIFNLRQSLNSVTQGVQWRN
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ORIGIN
Alignment Scores:
Pred. No.:      4,69e-142      Length:      1442
Score:      2034.00      Matches:      375
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0

US-09-380-203-2 (1-375) x AX774635 (1-1442)
Qy      1  MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20

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Db      15  ATGGAGTTTTCGCTCTTGTGTGCCAGGCTGGAGTGCATATGGCGCAATCTCAGCTCACCGC 74
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Db      75  AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCAGTAGTGGATT 134
Qy      41  ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
Db      135  ACAGCATGTGCAACCGCTCGGCTAATTTTGTATTTTATTTTATTTAGTAGAGATGGAGTT 194
Qy      61  LeuHisValGlyGlnAlaGlyLeuLeuProThrSerAspAspProSerValSerAla 80
Db      195  CTCCTATGTGGTCAGGCTGGTCTCGAATCCCGACCTCAGATGATCCCTCGCTCGCGCC 254
Qy      81  SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db      255  TCCCAAGTGTAGATACAGGACTGGCCACCATGCCCGGCTCTGCTGGCTAATTTTGT 314
Qy      101  GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLeuGlnSerThr 120
Db      315  GGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTCTGAGCTCAAGCAGTCCACC 374
Qy      121  CysLeuSerLeuProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
Db      375  TGCCTCAGCCTCCCAAGTGTGGGATTACAGGCGTGCAGCGCTGCGCTTTTATTT 434
Qy      141  LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db      435  TTAATTTTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTCAGTGGTGTGAT 494
Qy      161  HisSerSerLeuGlnProSerThrProGluLeuLeuHisProProAlaSerAlaSerGln 180
Db      495  CACAGCTCACTGCAGCCTTCAACTCTCAGATCAAGCATCTCTCTGCTGCTCAGCCTCCCAA 554
Qy      181  ValAlaGlyThrLeuAspMetHisIstYrThrTrpLeuLeuPheIlePheIlePheAsn 200
Db      555  GTAGCTGGGACCAAGACATGCACCATCACCTGGCTAATTTTTTATTTTATTTTAT 614
Qy      201  PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db      615  TTTTGTGACAGAGAGTCTCAACTCTGTCAACCGAGCTGGAGTGCAGTGGCGCAATCTTGGC 674
Qy      221  SerLeuGlnProLeuProGlyPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuSerSer 240
Db      675  TCACGTGCAACCTCTGCCTCCCGGTTCAAGTTATTTCTCTCCCGCAGCCTCTCTGAGTAGC 734
Qy      241  TrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
Db      735  TGGGACTACAGGCGCCACACCGCTAGCTAATTTTTTGTATTTTATTTAGTAGAGATGGGG 794
Qy      261  PheThrMetPheAlaArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280
Db      795  TTCACATGTTTCGCGAGGTTGATCTTGATCTCTGGACCTTGTGATCTGCTCGCTCGGCC 854
Qy      281  SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuLeuPheAsnPheCys 300
Db      855  TCCCAAGTGTGGGATTTACAGGCGTGAAGCACCACCGCCGCTTATTTTTTAATTTTGT 914
Qy      301  LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db      915  TTGTTTGAATGGAATCTCACTCTGTACCCAGGCTGGAGTGCATGGCAATCTCGGC 974
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Qy      341  TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db      1035  TGGGATTTAGGGACCTGCGCACACCGCCGCTAATTTTTTGTATTTTCAATTAGAGCGGG 1094
Qy      361  ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375

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Db      1095 GTTTCACCATATTGTGACGCTGGTCTCAAACTCTCTGACCTCAGG 1139
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BD070526      1442 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION Transgenic animals and cell lines for screening drugs effective for
the treatment or prevention of Alzheimer's disease.
ACCESSION BD070526
VERSION BD070526.1 GI:22616129
KEYWORDS JP 2001513777-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1442)
AUTHORS Monte,S.D. and Wands,J.R.
TITLE Transgenic animals and cell lines for screening drugs effective for
the treatment or prevention of Alzheimer's disease
JOURNAL Patent: JP 2001513777-A 1 04-SEP-2001;
COMMENT THE GENERAL HOSPITAL CORP
OS Unidentified
PN JP 2001513777-A/1
PD 04-SEP-2001
PR 26-FEB-1998 JP 1998537813
PR 26-FEB-1997 US 60/038908
PI SUZANNE DELA MONTE,JACK R WANDS
PC C07H21/02,C07H21/04,C12N5/00,C12N15/00,C12Q1/02,A61K48/00, PC
A61K49/00
CC Strandedness: Double;
CC Topology: Both;
CC Transgenic animals and cell lines for screening drugs CC
effective for the
treatment or prevention of Alzheimer's disease FH Key
Location/Qualifiers
FT CDS 15..1139.
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source
LOCATION/Qualifiers
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Alignment Scores:
Pred. No.: 4,69e-142 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCCGCTCAGCTGGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGCAATGTCACCCACACCTCGGCTAAATTTTGTATTTTGTAGTAGAGTGGAGTTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
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QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGCTAGATACAGGACTGGCCACCATGCGCGCTCTGCTGGCTAAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
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121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
375 TGCCCTCAGCCTCCCAAAGTGTGGGATTACAGCGGTGCAGCGCTGCTCGCCTTTTATT 434
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161 HisSerSerLeuGlnProSerThrProGluLysHisProAlaSerAlaSerGln 180
495 CACAGCTCACTGACGCTTCAACTCTCTGAGATCAAGCATCTCTGCTCAGCTCCCA 554
181 ValAlaGlyThrLysAspMethHisHisTyrThrTrpLeuIlePheIlePheAsn 200
555 GTAGCTGGGACCAAGACATGCACCATACCTGCTGCTAAATTTTATTTTATTTTAAAT 614
201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
615 TTTTGTAGACACAGTCTCAACTCTGTCAACCCAGGTGGAGTGCAGTGGCGCAATCTTGGC 674
221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
675 TCACCTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCCAGCTCTCTGAGTAGC 734
241 TrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
735 TGGGACTACAGCGGCCACCGCTAGCTAAATTTTGTATTTTGTAGTAGATGGGG 794
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795 TTCACCATGTTCCCGCAGGTGATCTGATCTCTGACCTTGTGATCTGCTCGCTCGGCC 854
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855 TCCCAAAGTGCTGGGATTACAGCGGTGAGCCACACCGCGCTTATTTTAAATTTTGT 914
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915 TTGTTTGAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCATGGCCAAATCTCGGC 974
321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
975 TCACCTGCAACCTCTCCCTCCCGGGCTCAAGCGATTCTCTGCTCAGCTCCCAAGCAGC 1034
341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAAATTTTGTATTTTTCATTAGAGCGGG 1094
361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
1095 GTTTCACCATATTGTGACGCTGGTCTCAAACTCTCTGACCTCAGG 1139
RESULT 11
AF010144      1442 bp      mRNA      linear      PRI 02-NOV-2001
LOCUS
DEFINITION Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.
ACCESSION AF010144
VERSION AF010144.1 GI:3002526
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1442)
AUTHORS Monte,S.M., Ghanbari,K., Frey,W.H., Beheshti,I., Averbach,P.,
Hauser,S.L., Ghanbari,H.A. and Wands,J.R.
TITLE Characterization of the AD7c-NTP cDNA expression in Alzheimer's
disease and measurement of a 41-kD protein in cerebrospinal fluid
JOURNAL J. Clin. Invest. 100 (12), 3093-3104 (1997)
MEDLINE 98064067
PUBMED 9399956

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REFERENCE
AUTHORS de la Monte,S.M. and Wands,J.R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1997) MGH Cancer Center, Massachusetts General
Hospital, 149 13th Street, Room 7308, Charlestown, MA 02129, USA
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QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
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QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTTTTTAAAGACACAGGTGTCCCACTCTTACCAGGATGAAGTAGAGTGGTGTAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGAGGCTTTCAACTCTGTAGATCAAGCATCTCTCTGCTCAGCTCCCAA 554

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QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTCCACGAGCTGGAGTGCAGTGGCGCAATCTTGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
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QY 241 TrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGGCCACACCGCTAGCTAAATTTTGTATTTTGTATTTAGTAGAGTAGGG 794
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Db 1035 TGGGATTACGGGCACCTGCCACACACCGCTAAATTTTGTATTTTATTTTATTTAGAGCGGG 1094
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RESULT 12
HS886K2/c
LOCUS
DEFINITION
Human DNA sequence from clone RP5-886K2 on chromosome 1p35.1-36.12
Contains elongin A (RNA polymerase II elongation factor),
hydroxymethylglutaryl-CoA lyase, GALE (UDP-galactose-4-epimerase)
ESTs, GSS, STS, CpG island, complete sequence.
ACCESSION
AL031295.1
VERSION
AL031295.1
KEYWORDS
HTG; elongin A; GALE; HMGCL; hydroxymethylglutaryl-CoA lyase; RNA
polymerase II elongation factor.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 124001)
Frankland,J.
Direct Submission
Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Mar 7, 1999 this sequence version replaced gi:4056542.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

RP5-886K2 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCIPAC2

This sequence is the entire insert of clone RP5-886K2.

FEATURES

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Location/Qualifiers

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327..594

/note="AluJb repeat: matches 1..294 of consensus"

597..863

/note="AluJo repeat: matches 5..298 of consensus"

868..1170

/note="AluYb8 repeat: matches 1..310 of consensus"

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/note="MIR repeat: matches 67..261 of consensus"

2288..2429

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2430..2714

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2728..3063

/note="L1M4 repeat: matches 2200..2535 of consensus"

3385..3686

/note="AluSx repeat: matches 1..310 of consensus"

3709..4050

/note="THE1C repeat: matches 1..371 of consensus"

4064..4212

/note="FRAM repeat: matches 1..155 of consensus"

4358..4506

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4788..4878

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5485..5653

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/note="L2 repeat: matches 1995..2748 of consensus"

7225..7293

/note="AluJb repeat: matches 152..220 of consensus"

7294..7753

/note="L2 repeat: matches 1543..1995 of consensus"

7756..8048

/note="AluSg repeat: matches 1..279 of consensus"

8050..8358

/note="AluY repeat: matches 1..309 of consensus"

8420..8987

/note="L2 repeat: matches 873..1539 of consensus"

8998..9090

/note="L2 repeat: matches 1543..1627 of consensus"

9060..9105

/note="L2 repeat: matches 827..872 of consensus"

9180..9279

/note="MIR repeat: matches 35..139 of consensus"

9489..9671

/note="MERSA repeat: matches 1..189 of consensus"

10530..10594

/note="L2 repeat: matches 2676..2750 of consensus"

10604..10678

/note="MIR repeat: matches 12..87 of consensus"

11227..11408

/note="MIR repeat: matches 20..232 of consensus"

11470..11776

/note="AluSx repeat: matches 1..311 of consensus"

12244..12546

/note="AluY repeat: matches 1..303 of consensus"

13021..13318

/note="AluSx repeat: matches 1..295 of consensus"

13319..13389

/note="MERSA repeat: matches 73..137 of consensus"

13390..13685

/note="AluSg repeat: matches 1..297 of consensus"

13686..13730

/note="MERSA repeat: matches 27..73 of consensus"

13759..13823

/note="L2 repeat: matches 2146..2215 of consensus"

13824..13959

/note="FLAM A repeat: matches 1..133 of consensus"

13960..14115

/note="L2 repeat: matches 2012..2146 of consensus"

14221..14479

/note="MER21B repeat: matches 156..456 of consensus"

14660..14709

/note="MIR repeat: matches 49..98 of consensus"

14953..15263

/note="AluSx repeat: matches 1..311 of consensus"

15508..15684

/note="MIR repeat: matches 2..218 of consensus"

15724..15857

/note="FLAM A repeat: matches 1..133 of consensus"

15961..16086

/note="FAM repeat: matches 12..163 of consensus"

16087..16394

/note="AluSg repeat: matches 3..310 of consensus"

16395..16409

/note="FAM repeat: matches 163..174 of consensus"

16722..16804

/note="L2 repeat: matches 2582..2691 of consensus"

16908..17483

/note="L1MB3 repeat: matches 5598..6185 of consensus"

17679..17881

/note="L2 repeat: matches 2285..2490 of consensus"

18516..18927

/note="MLTID repeat: matches 114..505 of consensus"

18928..19043

/note="FLAM C repeat: matches 1..116 of consensus"

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repeat_region 19044..19149
/note="MIR11D repeat: matches 6. .114 of consensus"
repeat_region 19750..20088
/note="L2 repeat: matches 2273. .2646 of consensus"
repeat_region 20092..20153
/note="31 copies 2 mer aa 80% conserved"
repeat_region 20170..20479
/note="AluX repeat: matches 3. .312 of consensus"
repeat_region 20499..20633
/note="L2 repeat: matches 2623. .2750 of consensus"
repeat_region 20639..20946
/note="AluX repeat: matches 1. .308 of consensus"
repeat_region 20959..21232
/note="AluX repeat: matches 1. .297 of consensus"
repeat_region 21240..21532
/note="AluSg repeat: matches 1. .293 of consensus"
repeat_region 21534..21837
/note="AluSp repeat: matches 2. .310 of consensus"
repeat_region 21839..21936
/note="MERSB repeat: matches 84. .175 of consensus"
repeat_region 21952..22283
/note="L2 repeat: matches 1811. .2198 of consensus"
repeat_region 22303..22605
/note="AluY repeat: matches 1. .301 of consensus"

Alignment Scores:
Pred. No.: 2,63e-122 Length: 124001
Score: 1799.00 Matches: 360
Percent Similarity: 94.52% Conservative: 2
Best Local Similarity: 93.99% Mismatches: 12
Query Match: 88.45% Indels: 11
DB: 9 Gaps: 2

US-09-380-203-2 (1-375) x HS886K2 (1-124001)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
DB 6072 ATGGAGTTTTCGCTCTTGTTGCCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACGCC 6013

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
DB 6012 AACCTCCGCTCCCGGGTTCAGCGATTCTCTGCTCAGCTCCCTAGTAGCTGGGATT 5953

QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
DB 5952 ACAGGCATGTGCCACACCGCTCGGCTAAATTTGTATTTTGTATTTTGTAGATGGAGTTT 5893

QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAla 80
DB 5892 CTCCTATGTTGGTCAGGCTGGTCTCGAATCCCGACCTCAGATGATCCTCCGCTCGGCC 5833

QY 81 SerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAlaAs 98
DB 5832 TCCCAAAGTGTGAGATT---ACAGGCATGAGCCACCATGCGCGCTCTGCTGGCTAA 5776

QY 98 nPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuIleYsG 118
DB 5775 TTTTGTGTGTAGAAACAGGGTTTCACTGATGTGTGCCAAGCTGGTCTCTGAGCTCAAGC 5716

QY 118 InSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArg--AlaAlaValProG1 137
DB 5715 AGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTACAGGCGTGAGCCACCGCTGCTGG 5656

QY 137 YLeuPheLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValG1 157
DB 5655 CTTTTTATTTATTTTATTTTAAAGACACACAGGTGTCCCACTTACCCAGGATGAAGTGA 5596

QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluIleLys-HisProProAlaAs 177
DB 5595 GTGGTGTATCAGCTACTCAGCCTTCACTCTGAGATCAAGCAATCTCTCGCT 5536

QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIleP 197

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Db 5535 CAGCTCCCAAGTAGCTGGGACCAAGACATGCACCATTACACCTGGGCTAATTTTATTT 5476
QY 197 heIlePheAsnPheLeuArgGlnSerLeuAnSerValThrGlnAlaGlyValGlnTrpA 217
Db 5475 TTATTTTAAATTTTGTAGACAGAGTCTCAC-TCTGTCCACCGAGCTGGAGTGCAGTGGC 5417
QY 217 rgAsnLeuGlySerLeuGlnProLeuProProGlyPheLysLeuPheSerCysProSerL 237
Db 5416 GCAATCTTGGGTCTCACTGCAACCTCTGCTCCGGGTTCAGGTATTTCTCTGCCCCAGCC 5357
QY 237 euLeuSerSerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuV 257
Db 5356 TCCTGAGTAGCTGGGACTACAGGCGCCACACCGCTAGCTAATTTTGTATTTTAG 5297
QY 257 alGluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeu 276
Db 5296 TAGAGATGGGGTTTCCACCATGTTCCGAGGTGGTCTTGATCTCTTGACCTTGATCTG 5237
QY 277 ProAlaSerAlaSerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIle 296
Db 5236 CTGCTCTCGGCTCCCAAAGTGTGGGATTACAGCGGTGAGCCACCGCGGCTATT 5177
QY 297 PheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrp 316
Db 5176 TTTAATTTTGTGTTGAAATGGAATCTCCTCTGTACCGAGCTGGAGTGCATGG 5117
QY 317 ProAsnLeuGlySerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSer 336
Db 5116 CACAATCTCGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGCGATTCTCTGTCTCAGC 5057
QY 337 LeuProSerSerTrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePhe 356
Db 5056 CTCCCAAGCAGCTGGGATTACGGGCACCTGCCAA--CACCCCGCTAAATTTTGTATTTTC 4999
QY 357 IleArgGlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 4998 ATTAGAGCGGGGTTTCCACATATTTGTGAGGCTGGTCTCAAACTCTCTGACCTCAGG 4942

RESULT 13
BD070528 1418 bp DNA linear PAT 27-AUG-2002
LOCUS Transgenic animals and cell lines for screening drugs effective for
DEFINITION the treatment or prevention of Alzheimer's disease.
ACCESSION BD070528
VERSION BD070528.1 GI:22616131
KEYWORDS JP 2001513777-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1418)
AUTHORS Monte,S.D. and Wands,J.R.
TITLE Transgenic animals and cell lines for screening drugs effective for
JOURNAL the treatment or prevention of Alzheimer's disease
PATENT: JP 2001513777-A 3 04-SEP-2001;
THE GENERAL HOSPITAL CORP
COMMENT OS Unidentified
PN JP 2001513777-A/3
PD 04-SEP-2001
PF 26-FEB-1998 JP 1998537813
PR 26-FEB-1997 US 60/038908
PI SUZANNE DELA MONTE, JACK R WANDS
PC C07H21/02, C07H21/04, C12N5/00, C12N15/00, C12Q1/02, A61K48/00, PC
A61K49/00
CC Strandedness: Both;
Topology: Both;
Transgenic animals and cell lines for screening drugs CC
effective for the
treatment or prevention of Alzheimer's disease FH Key
Location/Qualifiers 1. .1418
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FT source
Location/Qualifiers 1. .1418

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Best Local Similarity: 95.28% Mismatches: 1
Query Match: 87.86% Indels: 10
DB: 6 Gaps: 0

US-09-380-203-2 (1-375) x BD070528 (1-1418)

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QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 14 ATGGAGTTTTCGCTCTGTTGCCAGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 73

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProVal-AlaGlyIle 40
DB 74 AACCTCCGGCTCCCGGGTTCAGCGATTCTCTGCGCTCAGCCTCCCGAGTAGCTGGAT 133

QY 40 eThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPh 60
DB 134 TACAGGCATGTGCAC-CACGCTCGGCTAAATTTTGTATTTTATTTAGTAGAGATGGATT 192

QY 60 eLeuHisValGlyGlnAlaGlyLeuLeuLeuProThrSerAspAspProSerValSerAl 80
DB 193 TCTCCATGTTGTCAGCTGGTCTCGAATCTCCAGCTCAGATGATCTCCCGCTCTCGGC 251

QY 80 aSerGlnSerAlaArgTyrArgThrGlyHisAlaArg-LeuCysLeuAlaAsnPhC 100
DB 252 CTCCTCCAAAGTGTAGATACAGACTGAGCACCATGCCCCGGCTCTGCTGGCTAATTTT 311

QY 100 yGlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerT 120
DB 312 GTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGCTCAAGCAGTCCA 371

QY 120 hCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheI 140
DB 372 CTGCTCAGCTCCCGCTCCCAAGTGTGGAGTATACAGCGTGCAGCGCTGGCTTTTAA 431

QY 140 leLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
DB 432 TTTTATTTTATTAACACACAGGTGTCCCACTTTACCCAGGATGAAGTGCAGTGGTGTG 491

QY 160 sPHisSerSerLeuGlnProSerThrProGluLeuLysHisProAlaSerAlaSerG 180
DB 492 ATCAGAGCTCACTGCAGCCTTCAACTCT-GAGATCAAGCATCTCTGCTCAGCCTCCC 550

QY 180 ln-ValAlaGlyThrIleAspMetHisHisTyrThrTrpLeuLeuPheIlePheIlePhe 199
DB 551 AAGTAGCTGGGACCAACACATGACACCACTACACCTGGCTAATTTTATTTTATTTT 610

QY 200 AsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
DB 611 AATTTTGTAGACAGAGTCTCAACTGTGTACCCAGCTGGAGTGCAGTGGCGCAATCTT 670

QY 220 GlySerLeuGlnProLeuProProGlyPheLysLeuPheSerCysProSerLeuLeuSer 239
DB 671 GGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCGCCAGCTCTCTGAGT 730

QY 240 SerTrpAspTyrArgArgProArgLeuAlaAsnPhePheValPheLeuValGluMet 259
DB 731 AGCTGGGATACAGGCGCCACAGCCTAGCTAATTTTGTATTTTATTTAGTAGAGATG 790

QY 260 -GlyPheThrMetPheAlaArgLeuIleLeu-IleSerGlyProCysAspLeuProAlaAs 279
DB 791 GGGTTTACCAGTTCGCGCAGGTGTGATGTAGATCTCTTGACCTGTGTATCTGCTGCT 850

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DB 911 TTTTGTGTTTGTAAATGGAATCTCACTCTGTTTACCAGGCTGGAGTGCATGGCCAAAT 970

QY 319 LeuGlySerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuPro 338
DB 971 CTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGGATTCTCTCTCTCAGCTCCCA 1030

QY 339 SerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArg 358
DB 1031 AGCAGCTGGGATTACGGGCACCTGCA-CCACACCCCGCTAAATTTTGTATTTTCAATAGA 1089

QY 359 GlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
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AR051479
LOCUS AR051479 1381 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 49 from patent US 5830670.
ACCESSION AR051479
VERSION AR051479.1 GI:5974843
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1381)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease

JOURNAL Patent: US 5830670-A 49 03-NOV-1998;
FEATURES Location/Qualifiers

source
1..1381

ORIGIN
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 7.6e-104 Length: 1381
Score: 1520.00 Matches: 344
Percent Similarity: 90.16% Conservative: 4
Best Local Similarity: 89.12% Mismatches: 25
Query Match: 74.73% Indels: 22
DB: 6 Gaps: 3

US-09-380-203-2 (1-375) x AR051479 (1-1381)

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DB 74 AACCTCCGGCTCCCGGGTTCAGCGATTCTCTGCTCAGCCTCCCGAGTAGCTGGATT 133

QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
DB 134 ACAGGCATGTGCAC-CACGCTCGGCTAAATTTTGTATTTTATTTAGTAGAGATGGATT 192

QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerA 80
DB 193 AACTCAATGTTGGTCAGGCTGGTCTCGAATCTCCGACCTCAGATGATCTCCCGCTCTCGGC 252

QY 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
DB 253 CTGCCCAAAGTCTCAGATT---ACAGGCATGAGCCACCATGCCGGCTCTGCTGCTGCT 309

QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuL 117
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 QY 137 yLeuPheLeuPheLeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValG1 157
 Db 429 CTTTATTTATTTATTTTAAAGACACAGGTTGACCACTCTTCCAGGATGAAGTGCA 488
 QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuLys-HisProProAlas 177
 Db 489 GTGGTGTGATCAGCTCACTGAGCTTCAACTCTGAGATCAAGCAATCTCTGCTG 548
 QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisIstYrThrTrpLeuIlePheIleP 197
 Db 549 CAGCTTCCCAAGTAGCTGGGACCAAGACATGACCATCACCTACACCTGGTA-ATTTTATTT 607
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 QY 217 rgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
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 Db 964 GGCA-AATCTCGGTACTCGCAACCTCTCCCTCCCGGTC-AAGCGATTCTCTGTCTCA 1021
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 DEFINITION Sequence 49 from patent US 5948634.
 ACCESSION AR072619
 VERSION AR072619.1 GI:9999383
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1381)
 AUTHORS de la Monte, S. and Wands, J.R.
 TITLE Neural thread protein gene expression and detection of alzheimer's disease
 JOURNAL Patent: US 5948634-A 49 07-SEP-1999;
 FEATURES Location/Qualifiers
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 ORIGIN

Alignment Scores:
 Pred. No.: 7.6e-104 Length: 1381
 Score: 1520.00 Matches: 344
 Percent Similarity: 90.16% Conservative: 4
 Best Local Similarity: 89.12% Mismatches: 25
 Query Match: 74.73% Indels: 22
 DB: 6 Gaps: 3
 US-09-380-203-2 (1-375) x AR072619 (1-1381)
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 QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
 Db 74 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCCAGTAGCTGGATT 133
 QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
 Db 134 ACAGGATGTGCAC-CACGCTCGGCTAATTTTGTATTTTATTTAGTAGAGATGGAGTTT 192
 QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerA 80
 Db 193 AACTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATCTCCGCTCGGC 252
 QY 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
 Db 253 CTGCCCAAAGTCTGAGATT---ACAGGCATGAGCCACCATGCCCGGCTCTGCTGGCT 309
 QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuL 117
 Db 310 AATTTTGTGGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTCTCAGAGCTCA 369
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 QY 137 yLeuPheLeuPheLeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValG1 157
 Db 429 CTTTATTTATTTATTTTAAAGACACAGGTTGATCACTCTTACCCAGGATGAAGTGCA 488
 QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuLys-HisProProAlas 177
 Db 489 GTGGTGTGATCAACACTCACTGAGCTTCAACTCTCTGAGATCAAGCAATCTCTCTGCT 548
 QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisIstYrThrTrpLeuIlePheIleP 197
 Db 549 CAGCTTCCCAAGTAGCTGGGACCAAAAGACATGCACCATCACCTGGTA-ATTTTATTT 607
 QY 197 heIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
 Db 608 TTATTTTAAATTTTGTAGACAGAGTCTCAC-TCTGTCAACCCAGGCTGGAGTGCAAGTG 666
 QY 217 rgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
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 Db 727 TCTCAGTAGCTGGGACTACAGCGCCCCACCAAGCTAGCTAATTTTGTATTTTAG 786
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 QY 356 heIleArgGlyGlyValSerProTyrLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
 Db 1080 TCATTAGAGCGGGTTTA--CCATATTTGTAGGCTGGGTCTCAAACTCCTGACCTCAGG 1137

QY 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuS 336
Db 964 GGCA-AATCTCGGCTACTCGCAACCTCTGGCTCCCGGTC-AAGCGATTCTCTGTCTCA 1021
QY 336 erLeuProSerSerTrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIleP 356
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Db 1080 TCATTAGAGCGGGTTTA--CCATATTTGTAGGCTGGGTCTCAAACTCCTGACCTCAGG 1137

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Job time : 5498 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2005, 19:25:51 ; Search time 65 seconds
(without alignments)
2954.303 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLLPLRLCNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2034	100.0	375	2	O60448
2	595	29.3	587	1	ALU2_HUMAN
3	568	27.9	587	1	ALU3_HUMAN
4	549.5	27.0	591	1	ALU8_HUMAN
5	498.5	24.5	591	1	ALU1_HUMAN
6	389	19.1	585	1	ALU5_HUMAN
7	377.5	18.6	158	2	Q8NAL9
8	357.5	17.6	593	1	ALU6_HUMAN
9	356.5	17.5	603	1	ALU4_HUMAN
10	349	17.2	157	2	Q8N845
11	337.5	16.6	164	2	Q6ZTS0
12	332	16.3	176	2	Q6ZRS2
13	331	16.3	170	2	Q6ZV14
14	330.5	16.2	593	1	ALU7_HUMAN
15	325	16.0	143	2	Q6ZSJ7
16	320	15.7	195	2	Q6ZUW2
17	316	15.5	152	2	Q9NX85
18	303.5	14.9	239	2	Q6ZWA9
19	303	14.9	124	2	Q6ZVF6
20	301	14.8	156	2	Q8N266
21	295	14.5	193	2	Q6ZVX8
22	294.5	14.5	148	2	Q6ZUC5
23	290	14.3	123	2	Q6ZV58
24	287.5	14.1	166	2	Q6ZUC0
25	287	14.1	180	2	Q8N7M7
26	286.5	14.1	130	2	Q6ZSV2
27	286.5	14.1	131	2	Q6ZTD3
28	283	13.9	125	2	Q6ZTE1
29	281.5	13.8	147	2	Q6ZUA2
30	280	13.8	165	2	Q6ZTF6
31	279.5	13.7	132	2	Q6ZS28

32	279	13.7	142	2	Q6ZWD5	Q6zwd5 homo sapien
33	276	13.6	129	2	Q6ZW43	Q6zw43 homo sapien
34	274	13.5	125	2	Q8N8C2	Q8n8c2 homo sapien
35	274	13.5	164	2	Q6ZUK0	Q6zuko homo sapien
36	273.5	13.4	118	2	Q9H387	Q9h387 homo sapien
37	272	13.4	140	2	Q6ZU13	Q6zu13 homo sapien
38	271	13.3	121	2	Q6ZQS8	Q6zqs8 homo sapien
39	269	13.2	137	2	Q6ZS97	Q6zs97 homo sapien
40	269	13.2	241	2	Q6ZTY3	Q6sty3 homo sapien
41	268.5	13.2	129	2	Q6ZUW8	Q6zuw8 homo sapien
42	268	13.2	260	2	Q6ZQR8	Q6zqr8 homo sapien
43	267.5	13.2	165	2	Q6ZS53	Q6zs53 homo sapien
44	267.5	13.2	165	2	Q6ZT71	Q6zt71 homo sapien
45	267	13.1	120	2	Q6ZSU7	Q6zsu7 homo sapien

ALIGNMENTS

```

RESULT 1
O60448 PRELIMINARY; PRT; 375 AA.
AC O60448;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Neuronal thread protein AD7c-NTP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuronal;
RX MEDLINE=98064067; PubMed=9399956;
RA Monte S.M., Ghanbari K., Frey W.H., Beheshti I., Averbach P.,
RA Hauser S.L., Ghanbari H.A., Wands J.R.;
RT "Characterization of the AD7C-NTP cDNA expression in Alzheimer's
RT disease and measurement of a 41-kD protein in cerebrospinal fluid.";
RL J. Clin. Invest. 100:3093-3104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuronal;
RA de la Monte S.M., Wands J.R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF010144; AAC08737.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
SQ SEQUENCE 375 AA; 41720 MW; 955443950A5BFEFD CRC64;

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Query Match 100.0%; Score 2034; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-171;
Matches 375; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEFSLLPLRLCNGAISAHRNLRLPGSSDSDSPASPVAGITGCTHARLLLYFFLVMEF	60
Db	1	MEFSLLPLRLCNGAISAHRNLRLPGSSDSDSPASPVAGITGCTHARLLLYFFLVMEF	60
Qy	61	LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRRVSLMCPMSPELKQST	120
Db	61	LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRRVSLMCPMSPELKQST	120
Qy	121	CLSLPKCWYDYPRAAPVGLFILFLHRCPTTQDEVQWCDHSSLOPSTPEIKHPASASQ	180
Db	121	CLSLPKCWYDYPRAAPVGLFILFLHRCPTTQDEVQWCDHSSLOPSTPEIKHPASASQ	180
Qy	181	VAGTKDMHHYTLFIFIFLNFRLSLNSVTQAGVQWRNLGSLQPLPGKFLFSCPSLSS	240
Db	181	VAGTKDMHHYTLFIFIFLNFRLSLNSVTQAGVQWRNLGSLQPLPGKFLFSCPSLSS	240
Qy	241	WDYRRPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQSAAGITGVSHARLIFNFC	300

```

Db      241 WYRRPRLANFVFLVEMGFTMFARLLISGCDLPASASQAGITGVSHHARLIIFNC 300
QY      301 LFEMESHVSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
Db      301 LFEMESHVSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
QY      361 VSPYLSGWSQTPDLR 375
Db      361 VSPYLSGWSQTPDLR 375

```

RESULT 2

```

ALU2_HUMAN
ID ALU2_HUMAN STANDARD; PRT; 587 AA.
AC P39189;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SB sequence contamination warning entry.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA "The Alu family developed through successive waves of fixation closely
RA connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences

```

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CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U14568; -; NOT ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 96 Frame-1.
FT DOMAIN 100 194 Frame-2.
FT DOMAIN 198 292 Frame-3.
FT DOMAIN 296 391 Frame-4.
FT DOMAIN 395 489 Frame-5.
FT DOMAIN 493 587 Frame-6.
SQ SEQUENCE 587 AA; 63703 MW; 3EAA3E3E3929203 CRC64;
Query Match 29.3%; Score 595; DB 1; Length 587;
Best Local Similarity 41.5%; Fred. No. 5.7e-44;
Matches 153; Conservative 14; Mismatches 96; Indels 106; Gaps 8;
QY 6 LLPLRCNGAISAHNRNLRLPGSSDPASASPVAGITGMCTHARLLTYFFLVEMEFHYVQ 65
Db 304 LSPRLCSGSAISAHCKLRLPGSRHSPASASVAGTTGARHARLI-FVFLVETGHRVSQ 362
QY 66 AGLELPTSDPSVSASQASARYTGHARLCLANFCGRNRVSLMCPSPKQSTCLSLP 125
Db 363 DGLDLT-----XSAR-----RVHAILLPQPEXGLQAPATTP-----LGLP 378
QY 126 KCWDYRRAAVPGLFLLFRLHRCPTLTODEVQWCHSSLOSTPEIKHPASASQAVGK 185
Db 379 KCWDYRREPPRPAXXXFF-----XDGVSLLC-----RFGWSAVASRLTASSAS--- 421
QY 186 DMHHTYLIFIFIFNFLRQSLNSTVQAGVQWRNLGSLQPLPPGKFLFCPSLLSSWDYRR 245
Db 422 -----RVHAILLPQPEXGLQAPATTP----- 444
QY 246 PPRLANFVFLVEMGFTMFARLLISGCDLPASASQAGITGVSHHARLIIFNCLFEME 305
Db 445 ---CXFLYFXRRGFTVLARMVSTISXPRDPPASASQAGITGVSHRAXXX---FFETE 497
QY 306 SHSVTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGVSPYL 365
Db 498 SRVAQAGVQWRDLGSLQAPPPGFTPFCSLPSWDYRRPPRPANFCIFSRDGVSPGX 557
QY 366 SGWSQTPDL 374
Db 558 PGWSRSPDL 566
RESULT 3
ALU3_HUMAN
ID ALU3_HUMAN STANDARD; PRT; 587 AA.
AC P39190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SBI sequence contamination warning entry.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;

```

RT "Alu alert."; 6
 RL Nature 371:752-752 (1994).
 RN [2]
 RP CONCEPT.
 RX MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RL Genomics 12:838-841 (1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=88333009; PubMed=3138422;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation closely
 RT connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202 (1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121 (1991).
 CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
 CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
 CC consensus sequences have been constituted that contain all six
 CC frames conceptual translations of each of these classes of Alu
 CC repeats.
 CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
 CC codon, 'XXX' is used to separate the various translation phases.
 CC -!- CAUTION: This Alu entry is provided in order to avoid the further
 CC pollution of protein sequence databases with Alu-derived amino
 CC acid sequences.
 CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
 CC primate genomes with an average spacing of 4 kb. Some of them are
 CC actively transcribed by pol III. Normal transcripts may contain
 CC Alu-derived sequences in 5' or 3' untranslated regions. However,
 CC cDNA libraries also contain partial and/or rearranged cDNAs
 CC ligated with Alu-derived sequence in any orientation. Although Alu
 CC elements (especially situated on the complementary strand) have a
 CC great potential to create additional/alternative exons,
 CC consideration should be given to the possibility that the presence
 CC of an Alu in an open reading frame may have resulted from a
 CC cloning artifact or may be due to misinterpretation of sequencing
 CC data. This point has been overlooked on several occasions, with
 CC the consequence of erroneous Alu-derived amino acid sequences
 CC being reported.
 CC -!- CAUTION: Any significant similarity of a putative protein sequence
 CC with an Alu-translated entry must be taken as a warning that a
 CC part of Alu repeat may have been artifactually included in the
 CC coding nucleotide sequence.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U14569; -; NOT ANNOTATED_CDS.
 DR Hypothetical protein.
 KW DOMAIN 1 96 Frame-1.
 FT DOMAIN 100 194 Frame-2.
 FT DOMAIN 198 292 Frame-3.
 FT DOMAIN 296 391 Frame-4.
 FT DOMAIN 395 489 Frame-5.
 FT DOMAIN 493 587 Frame-6.
 SQ SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;
 Query Match 27.9%; Score 568; DB 1; Length 587;
 Best Local Similarity 41.5%; Pred. No. 1.4e-41;
 Matches 153; Conservative 15; Mismatches 95; Indels 106; Gaps 10;

QY 6 LLPLRLCNGAISAHNRNLRLPGSSDGPASAPVAGITGMCTHARLILYFLVEMFLRVGQ 65
 DB 304 LSPRLCECGGISAHCKLRLPGSRHSPASASQVAGITGARHYARLI-FVLVETGFRFSR 362
 QY 66 AGLELPTSDDPVSASQASARYFTGHARILCLANFCGRNVRVSLMCPSPWSPELKOSTCCLSLP 125
 DB 363 DGLDLTLT-----SXSAR-----LGLP 378
 QY 126 KCMYDERRAAVPGILFILFLRHRCPTLTODEVQCDHSSLOPSTPEIKHPASASQVAGTK 185
 DB 379 KCMYDERRRPPRAXXFF-----XDGVSLLC-----RCWNSA--VAGSR 414
 QY 186 DMHHTYTLIFIFINFLRQSLNSVTQAGVQWNLGSLQPLPGCFKLFCSPCLSSLDYRR 245
 DB 415 -----LTASSASRVHA-----ILLPQPKXGLQAPATTP----- 444
 QY 246 PPRLANFFVLVEMGFTMPARILILSGPCDLSPASASQASAGITGVSHHAKLIINFCLEFEME 305
 DB 445 ----GXFLYFXRRRGFTVLGAMVSIIXPRDPPASASQASAGITGVSHRAXXX---PFETE 497
 QY 306 SHSVTQAGVQWNLGSLQPLPGCLKRFCSCLSLPSSWDYGHLPHPANFCIFIRGGVSPYL 365
 DB 498 SRVSAQAGVQWRDLGSLQAPPGFTFFSCLSLPSSWDYRRPRLPANFCIFSRDGVSPFX 557
 QY 366 SCWSQTPDL 374
 DB 558 PCWSRSRSPDL 566
 RESULT 4
 ID ALU8 HUMAN STANDARD; PRT; 591 AA.
 AC P39195;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alu subfamily SX sequence contamination warning entry.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
 RA Claverie J.-M., Makalowski W.;
 RT "Alu alert.";
 RL Nature 371:752-752 (1994).
 RN [2]
 RP CONCEPT.
 RX MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RL Genomics 12:838-841 (1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=88333009; PubMed=3138422;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation closely
 RT connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202 (1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121 (1991).
 CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
 CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
 CC consensus sequences have been constituted that contain all six
 CC frames conceptual translations of each of these classes of Alu
 CC repeats.
 CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop

```

CC codon, 'XXX' is used to separate the various translation phases.
CC -! CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -! CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -! CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U14574; -; NOT ANNOTATED_CDS.
CC KW Hypothetical protein.
CC FT DOMAIN 1 96 Frame-1.
CC FT DOMAIN 100 195 Frame-2.
CC FT DOMAIN 199 294 Frame-3.
CC FT DOMAIN 298 393 Frame-4.
CC FT DOMAIN 397 492 Frame-5.
CC FT DOMAIN 496 591 Frame-6.
CC SQ SEQUENCE 591 AA; 64395 MW; AC8154AD8A6B280 CRC64;
CC
CC Query Match 27.0%; Score 549.5; DB 1; Length 591;
CC Best Local Similarity 38.9%; Pred. No. 6.1e-40;
CC Matches 150; Conservative 15; Mismatches 84; Indels 137; Gaps 11;
CC
CC Qy* 6 LPLRLECGAISAHNLRLPGSSDSPASASPVAGITGCMTHARLILYFPLVEMEFHVGQ 65
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 306 LSPRLCECGAISAHNLRLPGSSDSPASASRVAGITGARHARLI-FVFLVETGFHHVQ 364
CC
CC Qy 66 AGLELPTSD--PSVSASQASARYTGHARLCLANFCGRNRYSLMCPWS-----P 114
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 365 AGLELPTSDLPKVLGLQAXATAPQ----LRPXXXFFDXGVSCLRPGMSAVARSRLTAT 420
CC
CC Qy 115 ELKQSTCLSLPKCDW----YRRAAVPGLFILFLRHRCPTLTQDEVQWCDHSSLOPSPE 170
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 421 SASRVQAILLPQPEXGLQARATTPCXFLYFXRRGFTMLAR-----LVNSXPQ 471
CC
CC Qy 171 IKHPPASQVAGTKDMHHYTLIFIFIFNFLRQSLNSVTQAGVQWRNLGSLQPLPGPK 230
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 472 V-----IF----- 474
CC
CC Qy 231 LFSCLPSLLSSWDYRR-PPRLANFFVFLVEMGTFMFARLILISGPCDLPASASQSGAGITGV 289
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 475 -----LPKCWDYRREPP-----PASRXXX----- 495
CC
CC Qy 290 SHHARLIFNFCFLFEMESHVSTQAGVQWPNLGSLOPLPGLKRFSCLSLPSSWDYGHLP 349
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 496 -----PFETESRVAQAGVQWRDLGSLQPPPPGFKFSCLSLPSSWDYRRAPPR 544
CC
CC Qy 350 PANFCIFIRGGVSPYLSGWSQTPDLR 375
CC Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 545 PANFCIFIRSDGVSPCPGWSRTPDLR 570

```

```

RESULT 5
ALU1_HUMAN
ID ALU1_HUMAN STANDARD; PRT; 591 AA.
AC P39188;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily J sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -! MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
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CC codon, 'XXX' is used to separate the various translation phases.
CC -! CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -! CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
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CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
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CC being reported.
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CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC -----

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CC EMBL; U14567; -; NOT_ANNOTATED_CDS.

CC Hypothetical protein.

CC FT DOMAIN 1 96 Frame-1.

CC FT DOMAIN 100 195 Frame-2.

CC FT DOMAIN 199 294 Frame-3.

CC FT DOMAIN 298 393 Frame-4.

CC FT DOMAIN 397 492 Frame-5.

CC FT DOMAIN 496 591 Frame-6.

CC SEQUENCE 591 AA; 63790 MW; 665D395735519D95 CRC64;

Query Match 24.5%; Score 498.5; DB 1; Length 591;

Best Local Similarity 38.6%; Pred. No. 2e-35;

Matches 144; Conservative 15; Mismatches 103; Indels 111; Gaps 11;

QY 6 LLPRLECNAGISAHNRNLRPGSSDPSASAPVAGITGCTHARLILYFFLVMEFLHVGQ 65

DB 306 LSPRLCSCGATTAHCSLDLPGSSDPPASASRVAGTTGARHARLIFVFF-VETGPHYVAQ 364

QY 66 AGLELPTSDPSVASQSAARYRTG--HARLCLANFCGRNRYSLMCPSPSPKQSTCLS 123

DB 365 AGLELLGSSDPPASASQAGI-TGVSHRAR---XXFFXDRVSLCRPGWSA----- 411

QY 124 LPKCWDYRAAIVEGLFILFRLHRCPTLTQDEVQWCDHSLQSTPEIKHPASASQVAG 183

DB 412 -----VARSRLTAASTRAQ-----ALLPOPE----- 435

QY 184 TKDHHYTWLFIIFNRLQSLNSTVQGVQWRNLSLQIPPPGKFLSCPSLLSSWDY 243

DB 436 -----XLGLQAR-----ATTPG----- 447

QY 244 RPPRLANFVFLVEGFTMFARLILIS-GPCDLPASASQAGITGVSHHARLIFNFCFLF 302

DB 448 -----XFLYFLXRRGFTMLRVLNSNSWAQVILPPRPK---VLGLQAXATAPGXXXFF 497

QY 303 EMESHVSVTQGVQWPNLQSLQPLPGLKRFCSLSLPSWDYGHLPHPANFCIFIRGGVS 362

DB 498 ETGSRSAQAGVQWRDHGSLQRPPLKRSCLSLPSWDYRRAPRPNANFCIFCDGV 557

QY 363 PYLGSWQTPDLR 375

DB 558 LCCPGWRSRTPLGLK 570

RESULT 6

ALUS_HUMAN STANDARD; PRT; 585 AA.

AC P3192;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Alu subfamily SC sequence contamination warning entry.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RN SEQUENCE FROM N.A.

RP MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;

RA Claverie J.-M., Makalowski W.;

RT "Alu alert".

RL Nature 371:752-752(1994).

RN (2)

RN CONCEPT.

RA Claverie J.-M.;

RT "Identifying coding exons by similarity search: alu-derived and other

RT potentially misleading protein sequences".

RL Genomics 12:838-841(1992).

RN (3)

RN ALU FAMILIES CLASSIFICATION.

RX MEDLINE=88333009; PubMed=3138422;

RA Quentin Y.;

RT "The Alu family developed through successive waves of fixation closely

RT connected with primate lineage history.";

RL J. Mol. Evol. 27:194-202(1988).

RN (4)

RN ALU FAMILIES CLASSIFICATION.

RX MEDLINE=91178815; PubMed=1706781;

RA Jurka J., Milosavljevic A.;

RT "Reconstruction and analysis of human Alu genes.";

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CC being reported.

CC -!- CAUTION: Any significant similarity of a putative protein sequence

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CC -----

CC EMBL; U14571; -; NOT_ANNOTATED_CDS.

DR Hypothetical protein.

KW DOMAIN 1 95 Frame-1.

FT DOMAIN 99 193 Frame-2.

FT DOMAIN 197 291 Frame-3.

FT DOMAIN 295 389 Frame-4.

FT DOMAIN 393 487 Frame-5.

FT DOMAIN 491 585 Frame-6.

SQ SEQUENCE 585 AA; 63957 MW; 46E8C4F493650A7 CRC64;

Query Match 19.1%; Score 389; DB 1; Length 585;

Best Local Similarity 33.9%; Pred. No. 9.5e-26;

Matches 130; Conservative 23; Mismatches 100; Indels 130; Gaps 17;

QY 17 SAHRNLRPGSSDPSASAPVAGITGCTHARLILYFFLVMEFLHVGAGLELPTSDDP 76

DB 189 SVSKKXXPGAVAHACNPSLTGGRGRITRSR-----DRDHPGQHG-----ETP 232

QY 77 SVSASQSAARYRTGHHARLCLANFCGR-----NRV-----SLMC-PSWSPELKQST 120

DB 233 SILKTKLQAGRG--ARL-XSQLLGLRQENRNLPGGGSCSEPRSRHCTPAW-----RQSE 285

QY 121 CLSLPKCWDYRAAVPGLFILFRLHRCPTLTQDEVQWCDHSLQSTPEIKHPASASQ 180

DB 286 TPSQKK-----XXXFFLRSRL-----ALSPGW-----SA 309

QY 181 VAGTQDMHHYTWLIFIFNFIRQSLNSVTVQAGVQWRNGLSGLOLPP-----GPKLFSCPSL 237
 Db 310 VA-----RSRLTATSASRVQ-----AIILOPPPEXGLGQ----- 338
 QY 238 LSSWDYRRPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIF 297
 Db 339 -----ARATTSXFLYFXRRGFTMLARWVSIAPRDPASASQAGITGVSHHARXXX 392
 QY 298 NF-----CLFEMESHVTVQAGVQWRNGLSGLOLPPGLKRFCSLPSWDYDGHLPHPH 351
 Db 393 PFXDGVSLC-----RQAGVQWRDLGSLQPPPPGPKRFCSLPSWDYRRAPRPA 443
 QY 352 NFICFIRGVSVYLSGWSQTPDL 374
 Db 444 NFICFIRGVSVYLSGWSQTPDL 466

RESULT 7

Q8NAL9 PRELIMINARY; PRT; 158 AA.
 AC Q8NAL9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ35131.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murokami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK092450; BAC03893.1; --
 SQ SEQUENCE 158 AA; 17414 MW; E151503015F2FE34 CRC64;

Query Match 18.6%; Score 377.5; DB 2; Length 158;
 Best Local Similarity 53.3%; Pred. No. 2.2e-25;
 Matches 81; Conservative 7; Mismatches 21; Indels 43; Gaps 3;

QY 207 NSVTQAGVQWRNGLSGLOLPPGPKRFCSLSSWDYRR-PPRLANFFVFLVEMGFTMFA 265

Db 4 HSVTQAGVQWCGLSGLQLPLPPGPKRFFCLSSWDYRRVPPPLANFCIF----- 53
 QY 266 RLIIISGCDLPASASQAGITGVSHHARLIFNFCLEFEMESHVTVQAGVQWRNGLSGLOPL 325
 Db 54 -----FSF-FFEKESLSVTQAGVQWHDIGSLQAA 81
 QY 326 PPGLKRFCSLPSWDYDGHLPHPHPPANFCIFI 357
 Db 82 PPGFTFCSLPSWDYRRPPPCPFANFVFL 113
 RESULT 8
 ALU6 HUMAN STANDARD; PRT; 593 AA.
 AC P3193;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alu subfamily SP sequence contamination warning entry.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
 RA Claverie J.-M., Makalowski W.;
 RT "Alu alert.";
 RL Nature 371:752-752(1994).
 RN [2]
 RP CONCEPT.
 RX MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 potentially misleading protein sequences.";
 RL Genomics 12:838-841(1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=88333009; PubMed=3138422;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation closely
 connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
 into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
 consensus sequences have been constituted that contain all six
 frames conceptual translations of each of these classes of Alu
 repeats.
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 Alu-derived sequences in 5' or 3' untranslated regions. However,
 cDNA libraries also contain partial and/or rearranged cDNAs
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 great potential to create additional/alternative exons,
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U14572; -; NOT ANNOTATED_CDS.
 CC ProDom; PD003738; GIDA; 1.
 KW Hypothetical protein.
 FT DOMAIN 1 97 Frame-1.
 FT DOMAIN 101 196 Frame-2.
 FT DOMAIN 200 295 Frame-3.
 FT DOMAIN 299 395 Frame-4.
 FT DOMAIN 399 494 Frame-5.
 FT DOMAIN 498 593 Frame-6.
 SQ SEQUENCE 593 AA; 64603 MW; 136EF344AACD12A2 CRC64;
 Query Match 17.6%; Score 357.5; DB 1; Length 593;
 Best Local Similarity 48.2%; Pred. No. 5.9e-23;
 Matches 95; Conservative 6; Mismatches 47; Indels 49; Gaps 8;
 QY 4 SLLPLRLECNCAISAHNRLLPGSSDPASPVAGITGCTHARLLYFLVMEFLHV 63
 Db 405 SLLPLRLECNCAISAHNRLLPGSSDPASPVAGITGCTHARLLYFLVMEFLHV 463
 QY 64 GAGLEPLTSDPSVSASASARYTG--HARLCLANFCGRNVRSLMCPDWS-- 113
 Db 464 GAGLEPLTSDPSVSASASASAGI--TVSHRAR---XXFFETEFRCSCPGSAMARSRLT 519
 QY 114 -----PELQSTCLSLPKCWDYRRAAVPGLFILFLHRCPTLTQDEVQW 158
 Db 520 ATTSASRVQALLPQPEX-----LGLQAC-----ATTPGXFLYFXRRGFSMLVR----- 564
 QY 159 CDHSSLQSTPTPIKHP 175
 Db 565 ----LVNSRQVIRPP 577
 RESULT 9
 ID ALU4 HUMAN STANDARD; PRT; 603 AA.
 AC P39191;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alu subfamily SB2 sequence contamination warning entry.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
 RA Claverie J.-M., Makalowski W.;
 RT "Alu alert";
 RL Nature 371:752-752(1994).
 RN [2]
 RN CONCEPT.
 RP MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences."
 RL Genomics 12:838-841(1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.

RX MEDLINE=88333009; PubMed=3138422;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation closely
 RT connected with primate lineage history."
 RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
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 CC EMBL; U14570; -; NOT ANNOTATED_CDS.
 KW Hypothetical protein.
 FT DOMAIN 1 98 Frame-1.
 FT DOMAIN 102 199 Frame-2.
 FT DOMAIN 200 300 Frame-3.
 FT DOMAIN 304 401 Frame-4.
 FT DOMAIN 405 502 Frame-5.
 FT DOMAIN 506 603 Frame-6.
 SQ SEQUENCE 603 AA; 65272 MW; B8A0AD046BEA114 CRC64;
 Query Match 17.5%; Score 356.5; DB 1; Length 603;
 Best Local Similarity 30.3%; Pred. No. 7.3e-23;
 Matches 112; Conservative 28; Mismatches 115; Indels 115; Gaps 14;
 QY 76 PVSASQASRYRTGHARLCLANFCGRNVRSLMCPDWSPELQSTCLSLPKCWDYRRAAV 135
 Db 156 PSYWGXXRRMAXTREAEALVSRDCA---TAVRSPAWATERDSVS-----KQXXX 202
 QY 136 PGLFILFLHRC--PTLTQDEVQW-----DHSSLQSTP----- 169
 Db 203 PGA-----VACNCPSTLGGGWMRSGRDRHPCXQGETPSLLKIQISRARWAPVVP 257
 QY 170 -----EIKHP-----PASASQVAGTKMDHHYTWLIFIFINFLR 203
 Db 258 ATGEAAGEWREPGRKSLQXAEIAPLQSAVRPGRQSTPQSKKXKF-----FLR 307


```

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ46542.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Ninomiya K., Nagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128399; BAC87422.1; -.
SQ SEQUENCE 176 AA; 19060 MW; 9BD1CAC1940AD8FA CRC64;

Query Match 16.3%; Score 332; DB 2; Length 176;
Best Local Similarity 47.9%; Pred. No. 2.7e-21;
Matches 90; Conservative 11; Mismatches 51; Indels 36; Gaps 8;

QY 208 SVTQAGVQWNLGSLQPLPPGKFLFSCPSLLSSWDYRRPPRLAN-----PF 253
DB 5 SVSQAGVQWRD-----PPAHCIL---HLSSSD---SPASARVAVISGTCHHAQLIF 51

QY 254 VFLVEMGFTMFA-----RLILSGPCDLPASASQAGITGVSHARLIFNF-CLFEMESH 308
DB 52 VFLVETGFCVVGQAGLRLTSSDP---PTSASLSAGIAGLSHRAPFCFLCFVETVSH 108

QY 309 VTQAGVQWNLGSLQPLPGLKRFSCILPSSWDYCHLPPHPAN-FCIFRGVSPYLSG 367
DB 109 VTQNGQWCHDSQSRPPGLKRSPLLSSWDYRQASPHLANYFYFFIRGKSLCCPG 168

QY 368 WSQTDLR 375
DB 169 WSQTPELK 176

RESULT 13
Q62V14 PRELIMINARY; PRT; 170 AA.
AC Q62V14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ42545.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Ninomiya K., Nagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK124536; BAC85877.1; -.
SQ SEQUENCE 170 AA; 19351 MW; A019980274CEA078 CRC64;

Query Match 16.3%; Score 331; DB 2; Length 170;
Best Local Similarity 42.0%; Pred. No. 3.1e-21;
Matches 71; Conservative 16; Mismatches 38; Indels 44; Gaps 3;

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QY 251 NFFVFLVEMGFTMFAEL-----ILISGPCDLPASASQAGITG-----VSH 291
DB 2 NLLLPFKSQGLALLPRLKCSGAIHAHCNPELIGSSNFPDLASERAGTTAFGTWVLRISN 61

QY 292 HARLIFNF-----CLFEMESHVSTQAGVQWNLGSLQPLP 326
DB 62 HIAMLWDFFWRKQTIWSTRTLNHHHLVSCISPIIFETESHVSTQAGVQWNLSSLPQPP 121

QY 327 PGLKRFSCILPSSWDYCHLPPHPANFCIFRGVSPYLSGWSQTPDLR 375
DB 122 PGKRFSCILTPSTWDYQWMPCLANFCILFSDGVSYPWPGWSRTPDCR 170

RESULT 14
ALU7_HUMAN
ID ALU7_HUMAN STANDARD; PRT; 593 AA.
AC P39194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SQ sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=950211758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RL "Alu alert.";
RL Nature 371:752-752 (1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";
RL Genomics 12:838-841 (1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202 (1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121 (1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning consensus sequences have been constituted that contain all six frames conceptual translations of each of these classes of Alu repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing

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CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -I- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U14573; -; NOT ANNOTATED_CDS.
CC ProDom; PD003738; GIDA; 1.
CC KW Hypothetical protein.
CC FT DOMAIN 1 97 Frame-1.
CC 101 196 Frame-2.
CC FT DOMAIN 200 295 Frame-3.
CC FT DOMAIN 299 395 Frame-4.
CC FT DOMAIN 399 494 Frame-5.
CC FT DOMAIN 498 593 Frame-6.
CC SEQUENCE 593 AA; 64417 MW; 54A4F50F33A6089F CRC64;
CC -----
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Best Local Similarity 45.9%; Pred. No. 1.4e-20;
Matches 89; Conservative 9; Mismatches 53; Indels 43; Gaps 7;
QY 4 SLLPLRLCNGAISAHNRRLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEFLLHV 63
DB 405 SLLPLRLCNGAISAHNRRLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEFLLHV 463
QY 64 GQAGLELPTSDPSVSASQSAARYTG--HARLCLANFCGRNRVSLMCPSSWS----- 113
DB 464 GQAGLELPTSDPSVSASQSAARYTG--HARLCLANFCGRNRVSLMCPSSWS----- 113
QY 114 -----PELQSTQCLSLPKCKDYRRRAAVPGLFILFLRHRCPTLTQDEVQWCDH 161
DB 520 ATSASRVQAILLPQPEXILQLAP-----ATTGCFLYEXXRGFTMLAR----- 564
QY 162 SSLQPTPEIKHPP 175
DB 565 -LVSNSXPQVIHPP 577
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AC Q6ZSJ7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45460.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Subthalamic nucleus;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuno Y., Nagai K., Isegai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127382; BAC86951.1; -.
SQ SEQUENCE 143 AA; 15771 MW; AD4PBEFB10F6075C CRC64;
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Query Match 16.0%; Score 325; DB 2; Length 143;
Best Local Similarity 37.5%; Pred. No. 8.7e-21;
Matches 90; Conservative 9; Mismatches 39; Indels 102; Gaps 5;
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DB 6 FLULSPKLECGAILAHFNLCLLGSSDSPASASRVAGITGMHHRVRLI-FVFLVDTVY-Y 63
QY 63 VQAGLELPTSDPSVSASQSAARYTGTHARLCLANFCGRNRVSLMCPSSWSPELKQSTCL 122
DB 64 VQAGLELPTSD----- 76
QY 123 SLPKCKDYRRRAAVPGLFILFLRHRCPTLTQDEVQWCDHSSLPQSTPEIKHPPASASQVA 182
DB 77 -----LPASASQSA 85
QY 183 GTKDMHVTWLIFFIFENFLRQSLNSVTQAGVQWENLGSLOPLPPGFKLFSCPSLLSSWD 242
DB 86 GITGVSHCTWAPFFFFF-FLRQSF-IVIEAGVQWRDLSSLQLPPPGFPPFSCGLGLPSSWD 143
Search completed: September 13, 2005, 19:34:51
Job time : 67 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 18:32:09 ; Search time 272 Seconds
(without alignments)
8674.673 Million cell updates/sec

Title: US-09-380-203-1
Perfect score: 1442
Sequence: 1 TTTTTCGATGGAG.....TTAAACAAAGCTTTAGACGA 1442

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2.6/prodata/1/ina/5B COMB.seq:*
- 3: /cgn2.6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2.6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2.6/prodata/1/ina/PCUS COMB.seq:*
- 6: /cgn2.6/prodata/1/ina/backfilesi.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442	100.0	1442	2	US-08-454-557C-120
2	1442	100.0	1442	2	US-08-340-426D-120
3	1442	100.0	1442	2	US-08-450-673C-120
4	1442	100.0	1442	4	US-09-872-968-1
5	1223.4	84.8	1418	5	PCT-US95-17111A-120
6	1080.2	74.9	1381	2	US-08-454-557C-49
7	1080.2	74.9	1381	2	US-08-340-426D-49
8	1080.2	74.9	1381	2	US-08-450-673C-49
9	1080.2	74.9	1381	5	PCT-US95-17111A-49
10	590.4	40.9	42693	4	US-09-949-016-17317
11	590.4	40.9	42693	4	US-09-949-016-17318
12	597	36.5	107980	4	US-09-949-016-14370
13	519.6	36.0	39552	4	US-09-949-016-11799
14	506.4	35.1	13355	4	US-09-949-016-13162
15	502.4	34.8	43562	4	US-09-949-016-16222
16	499.2	34.6	100463	4	US-09-949-016-12511
17	499.2	34.6	100468	4	US-09-949-016-13725
18	493.2	34.2	84875	4	US-09-949-016-17334
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20	493.2	34.2	84875	4	US-09-949-016-17336
21	493.2	34.2	84875	4	US-09-949-016-17337
22	493.2	34.2	85152	4	US-09-949-016-12665
23	493.2	34.2	85152	4	US-09-949-016-12666
24	493.2	34.2	85152	4	US-09-949-016-12667
25	493.2	34.2	85152	4	US-09-949-016-12668
26	492.6	34.2	17198	4	US-09-949-016-13776
27	482	33.4	44477	4	US-09-949-016-16767

C	28	480.6	33.3	37269	4	US-09-949-016-16672	Sequence 16672, A
	29	479.6	33.3	57914	4	US-09-949-016-11935	Sequence 11935, A
	30	479.6	33.3	57936	4	US-09-949-016-16921	Sequence 16921, A
	31	479.2	33.2	51719	4	US-09-918-686-2	Sequence 2, Appli
	32	479.2	33.2	92139	4	US-09-918-686-1	Sequence 1, Appli
	33	478.8	33.2	12091	4	US-09-949-016-15805	Sequence 15805, A
C	34	477.6	33.1	60489	4	US-09-949-016-13716	Sequence 13716, A
	35	477.6	33.1	14452	4	US-09-949-016-16287	Sequence 16287, A
	36	475.8	33.1	107980	4	US-09-949-016-14370	Sequence 14370, A
	37	475.4	33.0	14796	3	US-08-975-080-35	Sequence 35, Appl
	38	475.4	33.0	14796	3	US-09-630-706-10	Sequence 10, Appl
	39	475.4	33.0	14796	3	US-09-496-694B-3	Sequence 3, Appli
	40	475.4	33.0	14796	4	US-10-138-618-35	Sequence 35, Appl
	41	475.4	33.0	14796	4	US-09-918-186A-3	Sequence 3, Appli
	42	474.8	32.9	30867	4	US-09-949-016-12231	Sequence 12231, A
	43	474.8	32.9	30868	4	US-09-949-016-13452	Sequence 13452, A
C	44	473.2	32.8	28806	4	US-09-949-016-13217	Sequence 13217, A
	45	473	32.8	91279	4	US-09-949-016-15146	Sequence 15146, A

ALIGNMENTS

RESULT 1
US-08-454-557C-120
; Sequence 120, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
US-08-454-557C-120

Query Match 100.0%; Score 1442; DB 2; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTTCGATGGAGTTTCGCTCTTTGCCAGGCTGGAGTGCATGGCGCAA 60

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1 TTTTCTTTTGTGAGTGGAGTTTTCGCTCTTGTGCCCCAGGCTGAGTGCATGSGGCA 60
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181 TAGAGATGAGTTTCTCCATGTTGCTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
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301 TGGCTAATTTTGTGTAGAAACAGGTTTCACTGATGTGCCAAGCTGCTCTCTGAGC 360
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361 TCAAGCAGTCCACCTCGCTCAGCTCCCAAGTGTGCGATTTACAGGCGTGCAGCGTGC 420
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421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTTGTCCTTACCCAGGATGAAG 480
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721 GCCTCTCAGTAGTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTTT 780
721 GCCTCTCAGTAGTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTTT 780
781 TAGTAGAGATGGGTTTCACTATTTGCGCAGGTTGATCTTGATCTCTGGACCTGTGATC 840
781 TAGTAGAGATGGGTTTCACTATTTGCGCAGGTTGATCTTGATCTCTGGACCTGTGATC 840
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901 TTTTATTTTATTTTGTGTTGAAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAT 960
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961 GGGCAATCTCGGCTCAGTGCACCTCTGCTCCCGGCTCAAGGATTTCTCTGCTCA 1020
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QY 1201 CGGCTTAATTTAGATAAAATAATATGATAGCAATGCGGGGTCTTGCTATGTTGCCAGGCT 1260
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Db 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACCAACCCAGCCAGTCA 1320
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Db 1381 CAAACCTGCAATTCAGTAGTAAACAGAGTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
QY 1441 CA 1442
Db 1441 CA 1442

RESULT 2

US-08-340-426D-120
; Sequence 120, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 15..1139
US-08-340-426D-120

Query Match 100.0%; Score 1442; DB 2; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	481	TGCAGTGTGTGATCAGAGTCACTGCGAGCTTCAACTCTCTGAGATCAAGCATCTCTG	540
Db	481	TGCAGTGTGTGATCAGAGTCACTGCGAGCTTCAACTCTCTGAGATCAAGCATCTCTG	540
QY	541	CCTCAGCTCCCAAGTGTGGACCAAGATGCACCATCACCTACACCTGGCTAATTTT	600
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QY	601	TTTTTATTTTTTATTTTTTATTTTTTAAAGACAGAGTGTCCCACTCTTACCCAGATGAGT	660
Db	601	TTTTTATTTTTTATTTTTTATTTTTTAAAGACAGAGTGTCCCACTCTTACCCAGATGAGT	660
QY	661	GGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATCTCTGCGCCA	720
Db	661	GGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATCTCTGCGCCA	720
QY	721	GCCTCTCAGTAGCTGGGACTACAGGCGCCACACAGCTAGCTAATTTTTTGTATTTT	780
Db	721	GCCTCTCAGTAGCTGGGACTACAGGCGCCACACAGCTAGCTAATTTTTTGTATTTT	780
QY	781	TAGTAGAGATGGGTTTCAACATGTTTGGCAGGTGATCTTGATCTCTGAGCTTGTGATC	840
Db	781	TAGTAGAGATGGGTTTCAACATGTTTGGCAGGTGATCTTGATCTCTGAGCTTGTGATC	840
QY	841	TGCTGCTCTGGCTCCCAAGTGTGGATTACAGGCGTGAAGCACCACCGCGGCTTA	900
Db	841	TGCTGCTCTGGCTCCCAAGTGTGGATTACAGGCGTGAAGCACCACCGCGGCTTA	900
QY	901	TTTTTATTTTTTGTGTTTGTGAATGGAATCTCACTCTGTTACCCAGGCTGGATGCAAT	960
Db	901	TTTTTATTTTTTGTGTTTGTGAATGGAATCTCACTCTGTTACCCAGGCTGGATGCAAT	960
QY	961	GGCCAAATCTCGGCTCACTGCAACCTCTGCGCTCCCGGCTCAAGGATTTCTCTGTCTCA	1020
Db	961	GGCCAAATCTCGGCTCACTGCAACCTCTGCGCTCCCGGCTCAAGGATTTCTCTGTCTCA	1020
QY	1021	GCCTCCCAAGCAGCTGGGATTACGGGCACTTGCACCAACACCCCGCTAATTTTGTATTT	1080
Db	1021	GCCTCCCAAGCAGCTGGGATTACGGGCACTTGCACCAACACCCCGCTAATTTTGTATTT	1080

RESULT 3

US-08-450-673C-120

; Sequence 120, Application US/08450673C

; Patent No. 5948888

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

; TITLE OF INVENTION: of Alzheimer's Disease

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,673C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; REFERENCE/DOCKET NUMBER: 0609.3840004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 120:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: both

; MOLECULE TYPE: cdna

; FEATURE:

; NAME/KEY: CDS

i	LOCATION: 15..1139									
	US-08-450-673C-120									
	Query Match 100.0%; Score 1442; DB 2; Length 1442;									
	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TTTTTTTTTTT	TGAGATGGAGTTT	TGCTCTT	GTGCCCAGGCT	GAAGTGC	AAATGGCGCA	60		
DB	1	TTTTTTTTTTT	TGAGATGGAGTTT	TGCTCTT	GTGCCCAGGCT	GAAGTGC	AAATGGCGCA	60		
QY	61	TCTCAGCT	CACGCAACCT	CCGCCCT	CCGGGTT	CAAGCGAT	TCTCT	CGCTCAGCCTCC	120	
DB	61	TCTCAGCT	CACGCAACCT	CCGCCCT	CCGGGTT	CAAGCGAT	TCTCT	CGCTCAGCCTCC	120	
QY	121	CAGTAGCTGGGAT	TACAGGCAT	TGTGC	CAACGCT	CGGCTA	ATTTTGT	ATTTTTTTAG	180	
DB	121	CAGTAGCTGGGAT	TACAGGCAT	TGTGC	CAACGCT	CGGCTA	ATTTTGT	ATTTTTTTAG	180	
QY	181	TAGAGATGGAGTT	TCTCCAT	GTGTG	CTCAGGCTGGT	CTCGA	ACTCCGACCT	CAGATGATC	240	
DB	181	TAGAGATGGAGTT	TCTCCAT	GTGTG	CTCAGGCTGGT	CTCGA	ACTCCGACCT	CAGATGATC	240	
QY	241	CCTCGCT	CTCGGCTCC	CAAGTGT	GATACAG	ACTGGCC	CAACAT	TGCCGCTCTGCC	300	
DB	241	CCTCGCT	CTCGGCTCC	CAAGTGT	GATACAG	ACTGGCC	CAACAT	TGCCGCTCTGCC	300	
QY	301	TGGCTAA	TTTTTGTG	TAGAAACAG	GGTTTCA	TGATG	TGCCAAGCT	TCTCTGAGC	360	
DB	301	TGGCTAA	TTTTTGTG	TAGAAACAG	GGTTTCA	TGATG	TGCCAAGCT	TCTCTGAGC	360	
QY	361	TCAAGCAGT	CCACCTGC	CTCAGCCT	CCCAAGT	GTCTGG	GAATAC	AGGCGTGCAGCGTGC	420	
DB	361	TCAAGCAGT	CCACCTGC	CTCAGCCT	CCCAAGT	GTCTGG	GAATAC	AGGCGTGCAGCGTGC	420	
QY	421	CTGGCT	CTTTTAA	TTTTTAA	GCACAG	GTGCTCC	ACTCTT	ACCCAGGATGAAG	480	
DB	421	CTGGCT	CTTTTAA	TTTTTAA	GCACAG	GTGCTCC	ACTCTT	ACCCAGGATGAAG	480	
QY	481	TGAGTGGT	GTGATC	ACAGCT	CACTG	CAGCTT	CAACT	CTGAGATCAAGCATCTCTCTG	540	
DB	481	TGAGTGGT	GTGATC	ACAGCT	CACTG	CAGCTT	CAACT	CTGAGATCAAGCATCTCTCTG	540	
QY	541	CCTCAGCCT	CCCAAGT	GTGGG	CCCAAG	AGATG	CAAC	CTACACCTGGCTAAATTTT	600	
DB	541	CCTCAGCCT	CCCAAGT	GTGGG	CCCAAG	AGATG	CAAC	CTACACCTGGCTAAATTTT	600	
QY	601	TTTTTAA	TTTTTAA	TTTTTAA	GCACAG	GTGCTCA	ACTCTG	TACCCAGGCTGGAGTGCAGT	660	
DB	601	TTTTTAA	TTTTTAA	TTTTTAA	GCACAG	GTGCTCA	ACTCTG	TACCCAGGCTGGAGTGCAGT	660	
QY	661	GGCGCA	ATCTGGCT	CACTG	CAACCT	CTG	CGCTCCG	GGTTCAAGTTATCTCTCGCCCA	720	
DB	661	GGCGCA	ATCTGGCT	CACTG	CAACCT	CTG	CGCTCCG	GGTTCAAGTTATCTCTCGCCCA	720	
QY	721	GCCTCT	GTAGTGGG	ACTAC	AGCGCC	CAAC	CTG	AGCTAGCTAAATTTTGTATTTT	780	
DB	721	GCCTCT	GTAGTGGG	ACTAC	AGCGCC	CAAC	CTG	AGCTAGCTAAATTTTGTATTTT	780	
QY	781	TAGTAGAG	TGGGTT	TACCAT	GTG	CCAGG	TTGAT	CTTGACCTCTGGACCTGTGATC	840	
DB	781	TAGTAGAG	TGGGTT	TACCAT	GTG	CCAGG	TTGAT	CTTGACCTCTGGACCTGTGATC	840	
QY	841	TGCTGCT	CTCGGCTCC	CAAGTGT	GGGAT	TAC	AGGCGT	AGCCAC	CGCCGGCTTA	900
DB	841	TGCTGCT	CTCGGCTCC	CAAGTGT	GGGAT	TAC	AGGCGT	AGCCAC	CGCCGGCTTA	900
QY	901	TTTTTAA	TTTTTGT	TGTAAT	TGAA	TGGA	ATCTC	ACTCTG	TACCCAGGCTGGAGTGCAT	960
DB	901	TTTTTAA	TTTTTGT	TGTAAT	TGAA	TGGA	ATCTC	ACTCTG	TACCCAGGCTGGAGTGCAT	960
QY	961	GGCCAA	ATCTCGGCT	CACTG	CAACCT	CTG	CGCTCCG	GGCTCAAGCGATTTCTCTGTCTCA	1020	
DB	961	GGCCAA	ATCTCGGCT	CACTG	CAACCT	CTG	CGCTCCG	GGCTCAAGCGATTTCTCTGTCTCA	1020	

Db	961	GGCCAAATCT	CGGCTAC	TCTGCA	CACTCTG	CCCTCCG	GGCTCA	AGCGATTTCT	CTCTGTCTCA	102
QY	1021	GCCTCCC	AAAGCAG	CTGGGAT	TACGGG	CAACCTG	CCACCA	CAACCCCGCTAA	TTTTTGTATTT	1080
Db	1021	GCCTCCC	AAAGCAG	CTGGGAT	TACGGG	CAACCTG	CCACCA	CAACCCCGCTAA	TTTTTGTATTT	1080
QY	1081	TCATTTAG	AGGCGGGG	TTTTTCA	CCATATTT	TGTCAGG	CTGGTCT	CAAACTCT	CTGACCTCAGGT	1140
Db	1081	TCATTTAG	AGGCGGGG	TTTTTCA	CCATATTT	TGTCAGG	CTGGTCT	CAAACTCT	CTGACCTCAGGT	1140
QY	1141	GACCCAC	CTGCCT	CAGCCTT	CCAAAGT	CTGGGAT	TACAGG	CGGTGAGC	CACTCACC	1200
Db	1141	GACCCAC	CTGCCT	CAGCCTT	CCAAAGT	CTGGGAT	TACAGG	CGGTGAGC	CACTCACC	1200
QY	1201	CGGCTAA	TTTTAG	ATAAAAA	ATATG	TAGCA	ATGGGG	GGTCTT	CTGTATGTTGCC	1260
Db	1201	CGGCTAA	TTTTAG	ATAAAAA	ATATG	TAGCA	ATGGGG	GGTCTT	CTGTATGTTGCC	1260
QY	1261	GGTCTCAA	AACTTCT	GGCTTCA	TGCAATCTT	CCAAT	TGAGCC	CAACAC	CCAGCAGTCA	1320
Db	1261	GGTCTCAA	AACTTCT	GGCTTCA	TGCAATCTT	CCAAT	TGAGCC	CAACAC	CCAGCAGTCA	1320
QY	1321	CATTTTTAA	ACAGTTA	CATCTT	TTATTTT	AGTATA	CTAG	AAAGTA	ATAAACAATG	1380
Db	1321	CATTTTTAA	ACAGTTA	CATCTT	TTATTTT	AGTATA	CTAG	AAAGTA	ATAAACAATG	1380
QY	1381	CAAACTC	CAAAATTC	AGTAG	TAACAG	AGTCTCTT	TATATA	CTTTTAA	CAAAAGCTTTAG	1440
Db	1381	CAAACTC	CAAAATTC	AGTAG	TAACAG	AGTCTCTT	TATATA	CTTTTAA	CAAAAGCTTTAG	1440
QY	1441	CA	1442							
Db	1441	CA	1442							

RESULT 4

US-09-872-968-1

Sequence 1, Application US/09872968

Patent No. 6770797

GENERAL INFORMATION:

APPLICANT: Wands, Jack R

APPLICANT: de la Monte, Suzanne M

TITLE OF INVENTION: Inhibition of Neurodegeneration

FILE REFERENCE: 21486-047

CURRENT APPLICATION NUMBER: US/09/872,968

CURRENT FILING DATE: 2001-06-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1442

TYPE: DNA

ORGANISM: Homo sapiens

US-09-872-968-1

Query Match 100.0%; Score 1442; DB 4; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTTTTTTTTTGAGATGGAGTTTTCGCTCTTGTGCCCAGGCTGGAGTGC

DB 1 TTTTTTTTTTTTGAGATGGAGTTTTCGCTCTTGTGCCCAGGCTGGAGTGC

QY 61 TCTCAGCTCACGCAACCTCCGCCCTCCGGGTTCAAGCGATTCTCTCGCTCAGCCTCC

DB 61 TCTCAGCTCACGCAACCTCCGCCCTCCGGGTTCAAGCGATTCTCTCGCTCAGCCTCC

QY 121 CAGTAGCTGGGATTAACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTT

DB 121 CAGTAGCTGGGATTAACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTT

QY 181 TAGAGATGGAGTTTCTCCATGTGTGCTCAGGCTGGTCTCGAACTCCGACCTCAGATG

DB 181 TAGAGATGGAGTTTCTCCATGTGTGCTCAGGCTGGTCTCGAACTCCGACCTCAGATG

QY 241 CCTCGCTCTCGGCTCCCAAGTGTGATACAGGACTGGCCACCATCGCGGCTCTGCC

DB 241 CCTCGCTCTCGGCTCCCAAGTGTGATACAGGACTGGCCACCATCGCGGCTCTGCC

QY 301 TGGCTAA

DB 301 TGGCTAA

QY 361 TCAAGCAGTCCACCTGCCTCAGCCTCCCAAGTGTCTGGATTAACAGGCGTGCAGCGTGC

DB 361 TCAAGCAGTCCACCTGCCTCAGCCTCCCAAGTGTCTGGATTAACAGGCGTGCAGCGTGC

QY 421 CTGGCTCTTTTAA

DB 421 CTGGCTCTTTTAA

QY 481 TGCAAGTGGTGTGATCACAGCTCACTGCAAGCTTCAACTCTGAGATCAAGCATCTCTCTG

DB 481 TGCAAGTGGTGTGATCACAGCTCACTGCAAGCTTCAACTCTGAGATCAAGCATCTCTCTG

QY 541 CCTCAGCCTCCCAAGTGTGGGACCAAGACATGACCACTTACACCTGGCTAAATTTT

DB 541 CCTCAGCCTCCCAAGTGTGGGACCAAGACATGACCACTTACACCTGGCTAAATTTT

QY 601 TTTTTTAA

DB 601 TTTTTTAA

QY 661 GGCGCAATCTTGCTCACTGCAACCTCTGCCTCCGGGTTCAAGTTATCTCTCGCCCA

DB 661 GGCGCAATCTTGCTCACTGCAACCTCTGCCTCCGGGTTCAAGTTATCTCTCGCCCA

QY 721 GCCTCTGTAGTGTGGGACTACAGCGCCCAACACAGCTAGCTAAATTTTGTATTTT

DB 721 GCCTCTGTAGTGTGGGACTACAGCGCCCAACACAGCTAGCTAAATTTTGTATTTT

QY 781 TAGTAGAGATGGGTTTACCATGTGCGCAGGTTGATCTTGATCTCTGGACCTGTGATC

DB 781 TAGTAGAGATGGGTTTACCATGTGCGCAGGTTGATCTTGATCTCTGGACCTGTGATC

QY 841 TGCTGCTCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGCCACCAAGCGCGGCTTA

DB 841 TGCTGCTCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGCCACCAAGCGCGGCTTA

QY 901 TTTTTTAA

DB 901 TTTTTTAA

QY 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCCTCCCGGGCTCAAGCGATTTCTCTGTCTCA

DB 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCCTCCCGGGCTCAAGCGATTTCTCTGTCTCA

Db	961	GGCCAAATCTCGGCTCACTGCAACCTCTCGCTCCCGGGCTCAAGCGATTTCTCTGTGTCTCA	1020
Qy	1021	GCCTCCCAAGCAGCTGGGATTTACGGGCACTGCGCACCTGCGCACCAACCCCGCTAAATTTTGTGTATTT	1080
Db	1021	GCCTCCCAAGCAGCTGGGATTTACGGGCACTGCGCACCAACCCCGCTAAATTTTGTGTATTT	1080
Qy	1081	TCATTTAGAGGCGGGGTTTTCACCATATTTTGTTCAGGCTGGTCTCAAACTCCTGACCTCAGGT	1140
Db	1081	TCATTTAGAGGCGGGGTTTTCACCATATTTTGTTCAGGCTGGTCTCAAACTCCTGACCTCAGGT	1140
Qy	1141	GACCCACCTGCTCAGCCTTCCAAAGTGTCTGGGATTTACAGGCGTGAGCCACCTCAACCCAG	1200
Db	1141	GACCCACCTGCTCAGCCTTCCAAAGTGTCTGGGATTTACAGGCGTGAGCCACCTCAACCCAG	1200
Qy	1201	CCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGGTCTTGCTATGTGTGCCAGGCT	1260
Db	1201	CCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGGTCTTGCTATGTGTGCCAGGCT	1260
Qy	1261	GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACACCCAGCCAGTCA	1320
Db	1261	GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACACCCAGCCAGTCA	1320
Qy	1321	CATTTTTTAAACAGTTTACATCTTTATTTTAGTATATCTAGAAAGTAAATACAATAAACATGT	1380
Db	1321	CATTTTTTAAACAGTTTACATCTTTATTTTAGTATATCTAGAAAGTAAATACAATAAACATGT	1380
Qy	1381	CAAACTGCAAAATTCAGTAGTAAACAGAGTCTTTTTATTAACTTTTTAAACAAAGCTTTTAGAG	1440
Db	1381	CAAACTGCAAAATTCAGTAGTAAACAGAGTCTTTTTATTAACTTTTTAAACAAAGCTTTTAGAG	1440
Qy	1441	CA 1442	
Db	1441	CA 1442	

RESULT 4

US-09-872-968-1

Sequence 1, Application US/09872968

Patent No. 6770797

GENERAL INFORMATION:

APPLICANT: Wands, Jack R

APPLICANT: de la Monte, Suzanne M

TITLE OF INVENTION: Inhibition of Neurodegeneration

FILE REFERENCE: 21486-047

CURRENT APPLICATION NUMBER: US/09/872,968

CURRENT FILING DATE: 2001-06-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1442

TYPE: DNA

ORGANISM: Homo sapiens

US-09-872-968-1

Query Match 100.0%; Score 1442; DB 4; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTTTTTTTTTTTTTCAGATGCGAGTTTTTCGCTCTTGTTGTGCCAGGCTGGAGTGCATATGGCGCAA	60
Db	1	TTTTTTTTTTTTTTCAGATGCGAGTTTTTCGCTCTTGTTGTGCCAGGCTGGAGTGCATATGGCGCAA	60
Qy	61	TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGGATTTCTCTGCTCAGCCTCCC	120
Db	61	TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGGATTTCTCTGCTCAGCCTCCC	120
Qy	121	CAGTAGCTGGGATTCAGACGATGTGCACCAACCTCGGCTAAATTTTCTATTTTTTTTAG	180
Db	121	CAGTAGCTGGGATTCAGGCAATGTGCACCAACCTCGGCTAAATTTTCTATTTTTTTTAG	180
Qy	181	TAGAGATGGAGTTTCTCCATGTTGGTCAGCTGGTCTCGAACTCCGACCTCAGATGATC	240
Db	181	TAGAGATGGAGTTTCTCCATGTTGGTCAGCTGGTCTCGAACTCCGACCTCAGATGATC	240

RESULT 4
US-09-872-968-1
; Sequence 1, Application US/09872968
; Patent No. 6770797
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872, 968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-968-1

Query Match 100.0%; Score 1442; DB 4; Length 1442;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TTTTTTTTTTT	TGAGATGGAGTTT	TGCTCTT	GTGCCCAGGCT	GAAGTGC	AAATGGCGCA	60	
DB	1	TTTTTTTTTTT	TGAGATGGAGTTT	TGCTCTT	GTGCCCAGGCT	GAAGTGC	AAATGGCGCA	60	
QY	61	TCTCAGCT	CACGCAACCT	CCGCCCT	CCGGGTT	CAAGCGAT	TCTCT	CGCTCAGCCTCC	120
DB	61	TCTCAGCT	CACGCAACCT	CCGCCCT	CCGGGTT	CAAGCGAT	TCTCT	CGCTCAGCCTCC	120
QY	121	CAGTAGCTGGGAT	TACAGGCAT	TGTGC	CAACGCT	CGGCTA	ATTTTGT	ATTTTTTTAG	180
DB	121	CAGTAGCTGGGAT	TACAGGCAT	TGTGC	CAACGCT	CGGCTA	ATTTTGT	ATTTTTTTAG	180
QY	181	TAGAGATGGAGTT	TCTCCAT	GTGTG	CTCAGGCTGGT	CTCGA	ACTCCGACCT	CAGATGATC	240
DB	181	TAGAGATGGAGTT	TCTCCAT	GTGTG	CTCAGGCTGGT	CTCGA	ACTCCGACCT	CAGATGATC	240

QY 241 CCTCCGCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCACTGCGGCTCTGCC 300
 DB 241 CCTCCGCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCACTGCGGCTCTGCC 300
 QY 301 TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC 360
 DB 301 TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC 360
 QY 361 TCAAGCAGTCCACCTCGCTCAGCTCCCAAGTGTGGGATACAGCGGTGACGCGCTGC 420
 DB 361 TCAAGCAGTCCACCTCGCTCAGCTCCCAAGTGTGGGATACAGCGGTGACGCGCTGC 420
 QY 421 CTGGCCCTTTTAAATTTTAAATTTTAAAGACACAGGTGTCCCACTCTTACCAGGATGAAG 480
 DB 421 CTGGCCCTTTTAAATTTTAAATTTTAAAGACACAGGTGTCCCACTCTTACCAGGATGAAG 480
 QY 481 TGCAGTGGTGTATACAGCTCACTGACGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
 DB 481 TGCAGTGGTGTATACAGCTCACTGACGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
 QY 541 CCTCAGCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGCTGCTAAATTTT 600
 DB 541 CCTCAGCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGCTGCTAAATTTT 600
 QY 601 TTTTAAATTTTAAATTTTAAATTTTGAACAGAGTCTCAACTCTCTGACCCAGGCTGGAGTGCAGT 660
 DB 601 TTTTAAATTTTAAATTTTAAATTTTGAACAGAGTCTCAACTCTCTGACCCAGGCTGGAGTGCAGT 660
 QY 661 GGGGCAATCTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTAAATTTCTCTGCCCCA 720
 DB 661 GGGGCAATCTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTAAATTTCTCTGCCCCA 720
 QY 721 GCTCTGAGTGTGGGACTACAGGCGCCACCAAGCTAGCTAAATTTTGTATTTT 780
 DB 721 GCTCTGAGTGTGGGACTACAGGCGCCACCAAGCTAGCTAAATTTTGTATTTT 780
 QY 781 TAGTAGAGTGGGTTTCAACATTTTCCCAAGTGTGATCTCTGACCTTGTGATC 840
 DB 781 TAGTAGAGTGGGTTTCAACATTTTCCCAAGTGTGATCTCTGACCTTGTGATC 840
 QY 841 TGCCTGCTCGGCTCCCAAGTGTGGGATACAGGCGTGAAGCAACAGCGCGGCTTA 900
 DB 841 TGCCTGCTCGGCTCCCAAGTGTGGGATACAGGCGTGAAGCAACAGCGCGGCTTA 900
 QY 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAT 960
 DB 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAT 960
 QY 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGGATTTCTCTGTCTCA 1020
 DB 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGGATTTCTCTGTCTCA 1020
 QY 1021 GCTTCCCAAGCTGGGATTAAGGGCACTGCGCAACACCCCGCTAAATTTTGTATTT 1080
 DB 1021 GCTTCCCAAGCTGGGATTAAGGGCACTGCGCAACACCCCGCTAAATTTTGTATTT 1080
 QY 1081 TCAATAGAGCGGGTTTCAACATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
 DB 1081 TCAATAGAGCGGGTTTCAACATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
 QY 1141 GACCCACCTCTGAGCTTCCAAAGTGTGGGATTAAGGCGTGAAGCAACCTCAAGGAG 1200
 DB 1141 GACCCACCTCTGAGCTTCCAAAGTGTGGGATTAAGGCGTGAAGCAACCTCAAGGAG 1200
 QY 1201 CGGGCTAAATTTAGATAAAAAATATAGCAATGGGGGTCTTGCTATGTGCCCCAGGCT 1260
 DB 1201 CGGGCTAAATTTAGATAAAAAATATAGCAATGGGGGTCTTGCTATGTGCCCCAGGCT 1260
 QY 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCCAACACCCAGGAGTCA 1320
 DB 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCCAACACCCAGGAGTCA 1320

QY 1321 CATTTTAAACAGTTACATCTTTATTTTAGTATATCTAGAAAGTAAATACATAAACATCT 1380
 DB 1321 CATTTTAAACAGTTACATCTTTATTTTAGTATATCTAGAAAGTAAATACATAAACATCT 1380
 QY 1381 CAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
 DB 1381 CAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
 QY 1441 CA 1442
 DB 1441 CA 1442
 RESULT 5
 PCT-US95-17111A-120
 ; Sequence 120, Application PC/TUS9517111A
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wands, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
 ; TITLE OF INVENTION: Detection of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/17111A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/340,426
 ; FILING DATE: 14-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609.3840002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 120:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1418 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 14...1418
 PCT-US95-17111A-120
 Query Match 84.8%; Score 1223.4; DB 5; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;
 QY 2 TTTTATTTTTCAGATGGAGTTTTCGCTCTTGTGCCCCAGGCTGGAGTGCATGGCGCAAT 61
 DB 1 TTTTATTTTTCAGATGGAGTTTTCGCTCTTGTGCCCCAGGCTGGAGTGCATGGCGCAAT 60
 QY 62 CTCAGCTCACCGCAACCTCCGCTCCCGGTTCAAGCGATTTCTCTGCTCAGCGCTCCCC 121
 DB 61 CTCAGCTCACCGCAACCTCCGCTCCCGGTTCAAGCGATTTCTCTGCTCAGCGCTCCCC 120
 QY 122 AGTA-GCTGGGATTAACAGGCAATGTGACCCAGCTCGGCTAATTTTGTATTTTATTTAG 180
 DB 122 AGTA-GCTGGGATTAACAGGCAATGTGACCCAGCTCGGCTAATTTTGTATTTTATTTAG 180

180 AGAGATGGAATTTAACTCCAGTGTGGTCAGGCTGCTCGAACTCCCGACCTCAGATGAT 239
 240 CCTCCGCTCGGCTCCCAAGTGTCT---AGATACAGGACTGGCCACCATGCCGG-CT 295
 240 CTCCTGCTCGGCTGCCCAAGTGTGAGATTACAGGATGAGCCACCATGCCGGCT 299
 296 CTCCTGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATG-TGCCCAAGCTGTCTC 354
 300 CTCCTGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGTCTC 359
 355 CTGAGCTCAAGCAGTCCAGCTGCTCAGCTCCCAAGTGTGGGATTTACAGCGGTGAG 414
 360 CTGAGCTCAAGCAGTCCAGCTGCTCAGCTCCCAAGTGTGGGATTTACAGCGGT-CHG 418
 415 CCGTGTGCTGCTGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGG 474
 419 CCGTGTGCTGCTGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGG 478
 475 ATGAAGTGCAGTGTGTATCAAGCTCACTGAGCTTCACTCTGAGATCAAGC-AT 533
 479 ATGAAGTGCAGTGTGTATCAAGCTCACTGAGCTTCACTCTGAGATCAAGCAAT 538
 534 CTTCTGCTGCTGCTGCTCCCAAGTGTGGGACCAAGACATGACCACTACCTGGCTA 593
 539 CTTCTGCTGCTGCTGCTCCCAAGTGTGGGACCAAGACATGACCACTACCTGG-TA 597
 594 ATTTTATTTTATTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGG 653
 598 ATTTTATTTTATTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGG 656
 654 GTGAGTGGCGCAATCTTGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCC 713
 657 GTGAGTGGCGCAATCTTGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCC 716
 714 TGCCCCAGGCTCTGAGTGTGGGACTACAGCGGCCACAGGCTAGCTAATTTTTT 773
 717 TGCCCCAGGCTCTGAGTGTGGGACTACAGCGGCCACAGGCTAGCTAATTTTTT 776
 774 GTATTTTATGATAGATGGG-TTACCACTGTTTGGCAGGTTGATCTGATCTCTGGACC 832
 777 GTATTTTATGATAGATGGGTTTACCACTGTTTGGCAGGTTGATCTGATCTCTGGACC 836
 833 TTGTGATCTGCTGCTGCTGCT-CCCAAGTGTGGGATTTACAGCGGTGAGCCACG 891
 837 TTGTGATCTGCTGCTGCTGCTGCTACCAAGTGTGGGATTTACAG-GTGCTGACTCCAC 894
 892 CCGGCTTATTTTAAATTTTGTGTGTGTTGAAATGGAATCTCACTGTGTACCGAGGTG 951
 895 GCGGCTTATTTTAAATTTTGTGTGTGTTGAAATGGAATCTCACTGTGTACCGAGGTG 954
 952 GAGTGCATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATCT 1011
 955 GAGTGCATGG-CAAACTCGGCTACTGCAACCTCTGCTCCCGG-TCAGCGATCT 1012
 1012 CTGTCTCAGCTCCCAAGCAGTGGGATTTACGGGCACTGCGCACCAACCCCGCTAAT 1071
 1013 CTGTCTCAGCTCCCAAGCAGTGGGATTTACGGG-ACCTGCACCAACCCCGCTAAT 1070
 1072 TTGTGATTTTCAATAGAGGGGGTTTACCAATATTTGTGAGGCT-GGTCTCAAACTCT 1130
 1071 TTGTGATTTTCAATAGAGGGGG--TTTACCAATATTTGTGAGGCTGGGTCTCAAACTCT 1128
 1131 GACCTCAGGTGACCAACCTGCTCAGCTTCCAAAGTGTGGGATTTACAGGGGTGAGCA 1190
 1129 GACCTCAGGTGACCAACCTGCTCAGCTTCCAAAGTGTGGGATTTACAGGGGTGAGCA 1188
 1191 CTTCAACCGCGGCTAATTTTATGATAAATAATTTGAGCAATGGGGGGTCTTGTCTATG 1250
 1189 CTTCAACCGCGGCTAATTTTGAATAAATAATTTGAGCAATGGGGGGTCTTGTCTATG 1246
 1251 TGCCAGGCTGTCTCAAACTTCTGCTTCAATGCAATCTTCCAAATGAGCCCAACACC 1310
 1247 TGCCAGGCTGTCTCAAACTTCTGCTTCAATGCAATCTTCCAAATGAGCCCAACACC 1306

QY 1311 CAGCAGTCACTTTTAAACAGTTTACATCTTTTATTTTAGTATATAGAAAGTAAACA 1370
 Db 1307 CAGCAGTCACTTTTAAACAGTTTACATCTTTTATTTTAGTATATAGAAAGTAAACA 1366
 QY 1371 ATAAACATGTCAAC 1385
 Db 1367 ATAAACATGTCAAC 1381

RESULT 7

US-08-340-426D-49
 ; Sequence 49, Application US/08340426D
 ; Patent No. 5948634
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wands, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; TITLE OF INVENTION: of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/340,426D
 ; FILING DATE: 14-NOV-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609.3840002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1381 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; US-08-340-426D-49

Query Match 74.9%; Score 1080.2; DB 2; Length 1381;
 Best Local Similarity 94.4%; Pred. No. 2.9e-296;
 Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;
 QY 2 TTTTCTTTTTCAGATGAGATTTTTCGCTCTGTTGGCCAGGCTGGAGTGCATATGGCGCAAT 61
 Db 1 TTTTCTTTTTCAGATGAGATTTTTCGCTCTGTTGGCCAGGCTGGAGTGCATATGGCGCAAT 60
 QY 62 CTCAGCTCACCGCAACCTTCCGCTCCCGGGTTCAAGCGATTTCTCTGCTCAGCTCCGCC 121
 Db 61 CTCAGCTCACCGCAACCTTCCGCTCCCGGGTTCAAGCGATTTCTCTGCTCAGCTCCGCC 120
 QY 122 AGTAGCTGGGATTTACAGCATGTGCACCGCTCGGCTAATTTTGTATTTTGTATTTTGTAGT 181
 Db 121 AGTAGCTGGGATTTACAGCATGTGCA-CCACGCTCGGCTAATTTTGTATTTTGTATTTTGTAGT 179
 QY 182 AGAGATGAGATTTT-CTCCATGTTGGTCAGGCTGTCTCGAACTCCCGACCTCAGATCAT 239
 Db 180 AGAGATGAGATTTTAACTCCATGTTGGTCAGGCTGTCTCGAACTCCCGACCTCAGATCAT 239
 QY 240 CCCTCCGCTCTCGGCTCCCAAAGTGTCT---AGATACAGGACTGGCCACCATGCCGG-CT 295

Db 300 CTGCTGGCTAAATTTTGTGGTAGAAACAGGGTTTCACTGATGTTGCCAAGCTGGTCTC 359
Qy 355 CTGAGCTCAAGCAGTCCAGCTGCTCAGCTCCAAAGTGTGGGATTACAGGCGTGCAG 414
Db 360 CTGAGCTCAAGCAGTCCAGCTGCTCAGCTCCAAAGTGTGGGATTACAGGCGT-CAG 418
Qy 415 CCGTGGCTGGCTTTTATTTATTTTATTTTATTTTAAAGACACAGGTTCCACTCTTACCAGG 474
Db 419 CCGTGGCTGGCTTTTATTTATTTTATTTTATTTTAAAGACACAGGTTACCCTCTTACCAGG 478
Qy 475 ATCAAGTGCAGTGGTGTGATCACAGTCTCACTGAGCCTTCAACTCTGAGTCAAGC-AT 533
Db 479 ATCAAGTGCAGTGGTGTGATCACAGTCTCACTGAGCCTTCAACTCTGAGTCAAGCAAT 538
Qy 534 CTTCTGCTCAGCTCCAGCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACTGGCTA 593
Db 539 CTTCTGCTCAGCTCCAGCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACTGG-7A 597
Qy 594 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 653
Db 598 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 656
Qy 654 GTGCACTGGGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCC 713
Db 657 GTGCACTGGGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCC 716
Qy 714 TGCCCGCAGCTCTGAGTAGCTGGGACTACAGGCGCCACAGCCTAGCTAATTTTTT 773
Db 717 TGCCCGCAGCTCTGAGTAGCTGGGACTACAGGCGCCACAGCCTAGCTAATTTTTT 776
Qy 774 GTATTTTATTTAGTAGAGTGGG-TTCAACATGTTGCGCAGGTTGATCTTGATCTTGACC 832
Db 777 GTATTTTATTTAGTAGAGTGGGTTTCAACATGTTGCGCAGGTTGATCTTGATCTTGACC 836
Qy 833 TTGTGATCTGCTGCTCCGCT-CCCAAGTGTGGGATTACAGGCGTGAGCCACCAG 891
Db 837 TTGTGATCTGCTGCTCCGCTCAACAGTGTGGGATTACAG--GTGCTGACTCCAC 894
Qy 892 CCGGCTATTTTATTTTATTTTGTGTTGTTGAAATGAAATCTCACTCTGTTACCAGGCTG 951
Db 895 GCGGCTATTTTATTTTATTTTGTGTTGTTGAAATGAAATCTCACTCTGTTACCAGGCTG 954
Qy 952 GAGTGAATGGCCAAATCTGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCT 1011
Db 955 GAGTGAATGG-CAAAATCTGGCTACTCGCAACCTCTGCTCCCGGG-TCAAGCGATTCT 1012
Qy 1012 CTTGCTCAGCTCCCAAGCAGTGGGATTACGGGCACTGCGCACACACACCGCGTAAAT 1071
Db 1013 CTTGCTCAGCTCCCAAGCAGTGGGATTACGGG--ACCTGCAACACACACCGCGTAAAT 1070
Qy 1072 TTTGATTTTTCATTAGAGCGGGTTTCAACATATTTGTCAGGCT-GGTCTCAAACTCCT 1130
Db 1071 TTTGATTTTTCATTAGAGCGGG--TTTACATATTTTGTGAGGCTGGGTCTCAAACTCCT 1128
Qy 1131 GACCTCAGGTGACCACTGCTCAGCTTCCAAAGTGTGGGATTACAGGCGTGAGCCA 1190
Db 1129 GACCTCAGGTGACCACTGCTCAGCTTCCAAAGTGTGGGATTACAGGCGTGAGCCA 1188
Qy 1191 CTTCAACAGCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGTCTTGTATGT 1250
Db 1189 CTTCAACAGCGGCTAAATTTGGAATAAAAAATATGTAGCAATGGGG--TCTGTATGT 1246
Qy 1251 TGCCCGAGGCTGGTCTCAAACTTCTGCTTCAATGCAATCTTCAATGAGCCACACACC 1310
Db 1247 TGCCCGAGGCTGGTCTCAAACTTCTGCTTCAATGCAATCTTCAATGAGCCACACACC 1306
Qy 1311 CAGCCAGTCAATTTTAAACAGTTACATCTTTTATTTTATTTAGTATCTAGAAAGTATACA 1370
Db 1307 CAGCCAGTCAATTTTAAACAGTTACATCTTTTATTTTATTTAGTATCTAGAAAGTATACA 1366
Qy 1371 ATAAACATGTCAAC 1385
Db 1367 ATAAACATGTCAAC 1381

RESULT 9

PCT-US95-17111A-49
; Sequence 49, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
PCT-US95-17111A-49

Query Match 74.9%; Score 1080.2; DB 5; Length 1381;
Best Local Similarity 94.4%; Pred. No. 2.9e-296;
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;
Qy 2 TTTTCTTTTGTGAGATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGGCGCAAT 61
Db 1 TTTTCTTTTGTGAGATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGGCGCAAT 60
Qy 62 CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 121
Db 61 CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 120
Qy 122 AGTACTGGGATTACAGGCATGTGCCACCGCTCGGCTAAATTTTGTATTTTGTAGT 181
Db 121 AGTACTGGGATTACAGGCATGTGCCA-CGCGCTCGGCTAAATTTTGTATTTTGTAGT 179
Qy 182 AGAGATGAGATTTT--CTCATGTTGGTTCAGGCTGTGCTCGAACTCCGACCTCAGATGAT 239
Db 180 AGAGATGAGATTTTAACTCAATGTTGGTTCAGGCTGTGCTCGAACTCCGACCTCAGATGAT 239
Qy 240 CCTCCGCTCTCGGCTCCCAAGTGTCT--AGATAAGAGTGGCCACCATGCCGCT 295
Db 240 CTCCCGCTCTCGGCTCCCAAGTGTCTGAGATTACAGGCATGAGCCACCATGCCGCT 299
Qy 296 CTGCGCTGTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATG-TGCCCAAGCTGTCTC 354
Db 300 CTGCGCTGTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTTGTCGCCAAGCTGTCTC 359


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QY 999 CTCACGCGATTCTCTGTCTCAGCTCCCAAGCGCTGGATTACGGGCACTGCCACCA 1058
Db 41127 TTCAAGCGAATCTCTCGCTCAGTCTCCCAAGTAGCTAGGACTACAGGCAATGTGCCACCA 41068
QY 1059 CACCCCGCTAAATTTTGTATTTTTCATTAGAGCGGGTTTCAACCATATTTGTGAGCTGG 1118
Db 41067 CGCCCGCTAAATTTTGTATTTTGTAGAGAGAGGTTTTCACCATTTGGCCAGACTGG 41008
QY 1119 TCTCAAACTCTGACCTCAGGTGACCCACTGCTCAGCTTCCAAAGTGTGGGATTAC 1178
Db 41007 TCTTGAATCTCTAACTTCAAGTGTATCCACCGCTCTGCTCCCAAGTGTGGGATTAC 40948
QY 1179 AGCGGTGAGCCACTCACCCAGC---GGCTAAATTTAGATAAAATAATATGCAATG 1234
Db 40947 AGGCATGAGCCACACACTGCGCTCTGCCCAACTAAATTAATAAATAATTTGTAGAGA 40888
QY 1235 GGGGGTCTGTATGTTGCCAGGCTGGTCTCAAACTTCTGGCTTCATGCAATCTCTCCA 1294
Db 40887 CAGGATCTCACTATGTTGCCAGACTGGTCTTGAACCTCTGGGCTTAAGGATCTGCTG 40828
QY 1295 AATGAGCCAC 1304
Db 40827 TCTCAGCCTC 40818
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RESULT 12

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US-09-949-016-14370/c
; Sequence 14370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14370
; LENGTH: 107980
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(107980)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14370
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Query Match 36.5%; Score 527; DB 4; Length 107980;
Best Local Similarity 71.2%; Pred. No. 2e-138;
Matches 915; Conservative 0; Mismatches 280; Indels 90; Gaps 13;
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QY 1 TTTTGTGAGTGGAGTTTTCGCTCTGTGTCACCCAGGCTGGAGTGCAGTGGCACGG 22789
Db 22848 TATTTATTTATGACACAGAGTCTTGCTCTGTCTGTCACCCAGGCTGGAGTGCAGTGGCACGG 22789
QY 61 TCTCAGCTCAGCGCAACTCCGGCTCCGGGTTCAAGCGATTCTCTGCTCAGCTCC 120
Db 22788 TCTCGGTTCACTGCAACCTCCGGCTCCAGGTTCAAAATGATTCTCTGCTTTAGCCTCT 22729
QY 121 CAGTAGCTGGATTACAGCATGTGCAACCCAGCTCGGCTAAATTTTGTATTTTGTAG 180
Db 22728 GAGTAGCTGGATTACAGGACGCAACCAACCCAGGCTAAATTTT---TGTATTTTGTAG 22672
QY 181 TAGAGATGGAGTTTCTCCATGTTGGTCTCGAAGTGTGGTCTCGAAGTGTGGGATGATC 240
Db 22671 TAGAGACGGGGTTTCAACCATTTTGGCCAGGCTGTTCTTGAAATTCCTGACTTC---GTGATC 22614
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QY 241 CCTCGTCTCGGCTCCCAAGTGTGTAGATACAGGACTGGCCACCATCGCGGCTCTGCC 300
Db 22613 CGCTGCTCAGCTCCCAAGTGTCT-----GGATTTACAGGCTGTAGCCACCACT 22560
QY 301 TGGCTAAATTTTGTGATAGAACAGGTTTCACTGATGTGCCCAAGCTG----- 349
Db 22559 GGCCTATTTATTTTGTGATGAGATGCTTGTCTGTGTGCCAGGCTGGACTGAGTGG 22500
QY 350 -----GTCTCTGAGCTCAAGCAGTCCACCTGCTCAGC-----GTGCCCTGCC 426
Db 22499 TGCCATCTTGGCTCACTCAACCTCTGGGTTTCAAGTGATTCTCTGCTGCTCAGC 22440
QY 384 CTCCTCAAGTGTGGGATTACAGGCTGCCAGC-----GTGCCCTGCC 426
Db 22439 GTCCCGAGTAGCTGGGATTACAGGCGCAAGCCACCATGCCCGGCTAAATTTTGTATTTCT 22380
QY 427 TTTTATTTTATTTTATTTTAAAGACACAGTGTCCCACTTTACCCAGGATGAAGTGCAGT 486
Db 22379 TTTTATTTTATTTTATTTTGTAGATGAGTCTCACTTGTGTGCCAGGCTGGAGTGCAC 22320
QY 487 GGTGTGATCAGAGCTCACTGAGCCCTTCAACTCTCTGAGATCAAGC-ATCTCTCTGCTCA 545
Db 22319 AGTGGATCTTGGCTCACTGCAACCTCTGCTCCCGGTTTCAAGCGATTCTCTCTGCCCTCA 22260
QY 546 GCCTCCCAAGTAGCTGGGACCAAGACATGACACCACTACACTGCTGCTGCTTATTTTAT--- 601
Db 22259 GCCTCCCGAGTAGCTGGGATTACAGGCGCAAGCCACCATGCGCGCTAAATTTTGTATTT 22200
QY 602 -TTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGCAGT 660
Db 22199 CTTTCTTTTATTTTGTAGATGAGTCTCACTTGTCACTGCTAGGCTGGAGTGCAC 22140
QY 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCGGTTCAAGTTATTTCTCTGCCCA 720
Db 22139 GGTGGATCTTGGCTCACTGCAACCTCTGCTCCCGGTTTCAAGCGATTCTCTCTGCCCTCA 22080
QY 721 GCCTCTGAGTAGCTGGGACTACAGGCGCCACCAAGGCTAGCTAAT-TTTTGTATTT 779
Db 22079 GCCTCTTGGTACCTGGGATTATAGATGCTGCGCAACCATGCGCGCTAAATTTTGTATTT 22020
QY 780 TTAGTAGAGA-TGGGTTTCACTGTCGAGGTTGATCTTGTATCTCTGACCT--TGT 836
Db 22019 GTAGTAGAGACAGGTTTCAACATATTGAAAGGCTGTCTCGAATCTCTGACCTCAGGT 21960
QY 837 GATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGGCTGAGCCACCAAGCCCGG 896
Db 21959 GATCTGCTGCTCAGCCTCCCAAGTGTGGGATTACAGGCTGAGCCACCAAGCCCGG 21900
QY 897 CTTAT-----TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATCCC 945
Db 21899 CTTTTTACTTTTATTTATTTATTTATTTATTTTGAACAGAGTCTCACTCTGTCACTC 21840
QY 946 AGGCTGGAGTGAATGGCCAAATCTCGCTCACTGCAACCTCTGCTCCCGGCTCAAGC 1005
Db 21839 AGGCTGGAGTGAATGGCCAAATCTCGCTCACTGCAACCTCTGCTCCCGGCTCAAGC 21780
QY 1006 GATCTCTGCTCAGCTCCCAAGCAGTGGGATTACAGGCACTGCGCACTGCCACCAAGCCCG 1065
Db 21779 GATCTCTGCTCAGCCTCAGCCTGAGTAGCTGGGACTATAGGCACTGCGCCACCAAGCCCG 21720
QY 1066 CTAATTTTGTATTTTATTTAGAGGGGGTTTCAACATATTTGTGAGGCTGCTCTCAA 1125
Db 21719 CTGATTTTGTG--TTTGTAGTAGAGAGGTTTCAACATTTTGTGAGGCTGCTCTGAA 21662
QY 1126 CTCTGAGCTCAGGTGAGCCACTCTGCTCAGCTTTCCAAAGTGTGGGATTACAGGCTG 1185
Db 21661 CCGCTGAGCTCA--TGATCGGCTGCTTGGCTCCCAAGTGTCTCGGATTACAGGCTG 21604
QY 1186 AGCCACCTCACCCAGCGGCTAATT 1210
Db 21603 AGCCACCCAGCCCTAATTTT 21579
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RESULT 13
US-09-949-016-11799/c
; Sequence 11799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11799
; LENGTH: 39552
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(39552)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11799

Query Match          36.0%; Score 519.6; DB 4; Length 39552;
Best Local Similarity   69.0%; Pred.No. 1.5e-136; Indels    42; Gaps    10;
Matches      871; Conservative     0; Mismatches    349;

Qy       Db        1 TTTT...TTTTGAGATGGAGTTTCGCCTTGTTGCCCGCAGGTGCAATGGCGCAA 60
           34421 TTTT...TTTTGAGATGGAG-TTTCACCTTGTTGCCCGCAGGTGCAATGGCGTGA 34363

Qy       Db        61 TTCAGCTCACGGAACTCCGCCTCCGGGTTCAAGCGATTCTCTGCTCAGGCTCCC 120
           34362 TCCTCATVTCACCGAACCTCCGCCTTC CAGGTTCAACCGATTCTCTGCTCAGGCTCCC 34303

Qy       Db        121 CAGTAGCTGGGATTACAGGCATGTGCACCACGCTCGGCTAATTTTGTATTTTTTTTAG 180
           34302 AGTAGCTGGGACTACAGGCATGGCCACCACTGGCTTAATTTGTAT----TTTAG 34247

Qy       Db        181 TAGAGATGGAGTTTCTCCAATGTGTGTCAGGCTGGTCTCGAACTCCCGACCTCAGAATGATC 240
           34246 TAGAGACGGGCTTTCTCCATGTGTGTCAGGCTGGTCTTGAACCTCCCAACCTCAGGTGAT 34187

Qy       Db        241 CCTCGTCTCGGCTCCCAAGTGTAGATA CAGGACTGGGCCACCATGCCGCGCTCTGCC 300
           34186 CACTGGGCTTCGGCTCTCTAAAGT -ATTGAGATTACAGCGTGAAGCCACCGCGCTGGCT 34128

Qy       Db        301 TGGCTAATTTTGTGTAGAAAACAGGGTTTCACTGATGTGCCCAAGCTGTC-----TC 354
           34127 AATTTTGTATTTTATAGAGATGGGTTTTGCCATGTTGGCAGCGTGGTCTCAATTC 34068

Qy       Db        355 CTGAGCTCAACGATGCCACTGCTCAGCTCCCCAAAGTGTGGGATTACAGGCGTGCGAG 414
           34067 CTGACCTCAAGTGATCCACCGGCTTGCTCTCCAAAGTGTGGGATTACAGGCGTGATC 34008

Qy       Db        415 CGGTGCTCGGCTTTTATTTTATTTTATTTTAAAAAGACAAGGTGTCCCACTTTACCAGG 474
           34007 CACCATGCCGACGCTTCAATCTTTTCAAAGCTGAATAATTTCACATATATGTATAACC 33948

Qy       Db        475 ATGAAGTGCAGTGGTGTGATCACAGCTCACTGCGACCTTTCAACTCTGAGATCAAGCATC 534
           33947 ACATTGTTATCTATCCATCTGATGATAGTAGCTACCTGGGGTGTGTTCCAAATTTTAAATTT 33888

Qy       Db        535 CTCCTGCTCAGCCTCCCAAGTAGCTGGGACAAAGACATGCACCACCTACACCTGGCTAA 594
           33887 TAA'TTATTTTGTGTTTCATTTTATTTTA -----TTTTCT 33852

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US-09-949-016-13162

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Query Match      35.1%; Score 506.4; DB 4; Length 13335;
Best Local Similarity 71.0%; Pred. No. 5e-133;
Matches 887; Conservative 0; Mismatches 306; Indels 57; Gaps 14;

QY 1 TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 60
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 61 TCTCAGCTCAGCGCAACCTCCGCCCTCCCGGGTTCAAGCGATTCTCTGCTCAGCGCTCCC 120
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 3426 TATTGCCCTCAGTGCACCTCCGCCCTCCCGGGTTCAAGCGATTCTCTGCTCAGCGCTCCC 3485
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 121 CAGTAGCTGGGATTAAGGCAATGTCACCCAGCTCGGCTAAATTTGTAATTTTTCAGT 180
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QY 3662 -----TGTATTTTAGTAGAAGGGTTTTCACCATATTTGGCCAGGCTGGTTTCAAA 3712
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 352 CTCTGAGCTCAAGCAGTCCACTCGCTCAGCTCCCAAGTGTGGGATTAACAGCGTG 411
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QY 3713 CTCTGAGCTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3772
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

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QY 3934 CCAA-GTTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3990
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Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

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Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 4051 TCTCTGCCAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4110
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 769 TTTTATTTTTCAGATGAGTGGG-GTTTCACTGTTTCGCCAGAGTGTGATCTTGTATCT 827
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QY 828 GACCTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 887
Db TTTTATTTTTCAGATGGAGTTTCCTCTCTGTCGCCAGAGCTGGAGTGCATGGCGCAA 3425

QY 4171 TGACCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4230
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QY 888 CAGCGCCGCGC-----TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 941
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QY 4231 TGGCGCCGCGCCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 4290
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RESULT 15

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US-09-949-016-16222/c
; Sequence 16222, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16222
; LENGTH: 43562
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(43562)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16222

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Query Match      34.8%; Score 502.4; DB 4; Length 43562;
Best Local Similarity 69.4%; Pred. No. 1.2e-131;
Matches 861; Conservative 0; Mismatches 326; Indels 53; Gaps 11;

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QY 61 TCTCAGCTCAAGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCC 120
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QY 6715 TCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCC 6656
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QY 121 CAGTAGCTGGGATTAAGGCAATGTCACCCAGCTCGGCTAAATTTTGTATTTTTCAGT 180
Db TTTTATTTTTCAGATGGAGTTTTCGCTCTCTGTTGCCAGGCTGAGTGCATGGCGCAA 6600

QY 181 TAGAGATGGAGTTTTCATGTTGGTTCAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
Db TTTTATTTTTCAGATGGAGTTTTCGCTCTCTGTTGCCAGGCTGAGTGCATGGCGCAA 6540

QY 241 CTTCTCGTCTCGGCTCCCAAGTGTAGATACAGAGCTG---GCCACCATGCCGCTCT 297
Db TTTTATTTTTCAGATGGAGTTTTCGCTCTCTGTTGCCAGGCTGAGTGCATGGCGCAA 6480

QY 6539 TGACCGCTCTGCGCTCCCAAGTGTAGATACAGAGCTGTTTCACTGATGTGCCAAGCTGCTCTG 357
Db TTTTATTTTTCAGATGGAGTTTTCGCTCTCTGTTGCCAGGCTGAGTGCATGGCGCAA 6480

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Db 6479 TAAATCCTCATTTATATAATCAACTAAAGGAGTGTCTACTCTGTGTTTTTTCAATTCATACCT 6420
QY 358 AGCTCAAGCAGTCCACTGCTCAGCCTCCAAAGTGTGGGATT-----ACAGGCGTG 411
Db 6419 ATATGGAAGAAGAAAGTAGTAGTGAAGAAAGCATGGCTACATATCAGAAAACCTGGGAT 6360
QY 412 CAGCCGTGCTGGCCTTTTATTTTATTTTATTTTAAAGACACAGGTGCCACTCTTTACCC 471
Db 6359 CTGAATTTTCTGACAAATTTACACTACTTTTGTAGCATTAAGCCCTGGTGGTAATAAAC 6300
QY 472 AGGATGAAGTGCAG--TGGTGTGATCAGACTCAGCTGAGCCTTCAACTCCTGAGATCAA 529
Db 6299 AGCTAAGTGTCTGGAAGAAATATGATAAATCAGTACTACTAACAAGACTGGACATGTG 6240
QY 530 GCATCCTCTGCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTG 589
Db 6239 AGTTTGCACTGCTTATTAGGCTTTATGCTCTGTCTTAGGA-----TTTCTTTT 6190
QY 590 GCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 649
Db 6189 TCTTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 6131
QY 650 TGGAGTGCAGTGGCGCAATCTGGCTCAGTGCACCTCTGCTCCCGGTTCAAGTTATT 709
Db 6130 TGGAGTGCAGTGGCGCAATCTGGCTCAGTGCACCTCTGCTCCCGGTTCAAGTTATT 6071
QY 710 CTCCTGCCCGCAGCCTCCTGAGTAGCTGGGACTACAGGCGC---CCACACGCTAGCTAA 766
Db 6070 CTCCTGCCCTCAGCCTCCGATTTAGCTGGGACTACAGGCACTGCGCACCGCCCGGCTAA 6011
QY 767 TTTTATTTGTTATTTTATTTAGTAGATGG-----GGTTTCAACATGTTCTG 807
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QY 808 CCAGGTTGATCTTGATCTCTGACCTTTGATCTGCTGCTCCGCTCCGAAAGTCTG 867
Db 5950 GAGGTCAGGTCGTGATCTCTGACCTCGTGTATCCACCGCCTCGGCTCCCAAGTCTG 5891
QY 868 GGAATTACAGCGGTGAGCCACACCGCCCGG--CTTATTTTAAATTTTGTGTTGTAAT 925
Db 5890 GGAATTACAGGCATGAACCAACCGGCGCCGGCTTCTTTTCTTTTATTTTATTTTATTTT 5831
QY 926 GGAATCTCACT-CTGTTACCCAGGCTGGAGTGCAATGGCCAAATCTCGGCTCACTGCAAC 984
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QY 985 CTCTGCTCCCGGCTCAAGCGATCTCTGCTCTGAGCTCCAGCAGCAGCTGGATTAG 1044
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QY 1045 GGCACCTGCCACCAACCGCTTAATTTTGTATTTTATTTAGAGCGGGTTTCACCAT 1104
Db 5710 GGCATGTGCACCTGCGCCAGCTAATTTTGTATTTTATTTAGTAGAGTGGGTTTCTCCAT 5651
QY 1105 ATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGTGACCCACCTGCTCAGCCTTCCAA 1164
Db 5650 GTTGTGTCAGGCTGGTCTCAAACTCCCGACCTCAGATGATGACCTGCTCGGCTCCCGAG 5591
QY 1165 AGTGTGGGATTTACAGCGGTGAGCCACCTCACCCAGCCGG 1204
Db 5590 AGTGTGGGGTTCACAGCGGTGAGCCACTGGGCGCGGCTG 5551

Search completed: September 15, 2005, 22:21:10
Job time : 283 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 14:57:42 ; Search time 5116 Seconds
(without alignments)
10728.827 Million cell updates/sec

Title: US-09-380-203-1
Perfect score: 1442
Sequence: 1 TTTTITTTTGGATGAGGAG.....TTAAACAAAGCTTTAGACA 1442

Scoring table: IDENTITY_NUC
Gapop_10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	521.8	36.2	622	CA437412	CA437412 UI-H-DT0-
2	460.6	31.9	3016	BC068461	BC068461 Homo sapi
3	446.8	31.0	549	BM996475	BM996475 UI-H-DT0-
4	396.2	27.5	1842	BC011119	BC011119 Homo sapi
5	391.4	27.1	877	AQ739838	AQ739838 HS_5505_A
6	384.6	26.7	4191	AL832992	AL832992 Homo sapi
7	383.6	26.6	1345	AV762220	AV762220 AV762220
8	379.9	26.3	910	BQ722917	BQ722917 AGENCOURT
9	378.4	26.2	767	AV700498	AV700498 AV700498
10	377.6	26.2	613	CD709038	CD709038 EST25565
11	377.6	26.2	2097	CR614786	CR614786 full-length
12	377.4	26.2	604	CA439577	CA439577 UI-H-DT0-
13	376.4	26.1	628	CD690152	CD690152 EST6675 h
14	375.8	26.1	820	BUS68843	BUS68843 AGENCOURT
15	375.4	26.0	2777	HS8802772	HS8802772 Homo sapi
16	374.8	26.0	782	EX644719	EX644719 DKF2p781N
17	374.2	26.0	600	CA439719	CA439719 UI-H-DT0-
18	373.8	25.9	658	AQ393450	AQ393450 CITR1-E1
19	373	25.9	911	AQ746594	AQ746594 HS_2278_A
20	370.2	25.7	682	EX481615	EX481615 DKF2p686A
21	370	25.7	637	BQ438614	BQ438614 AGENCOURT
22	368.8	25.6	970	BM468547	BM468547 AGENCOURT
23	367.6	25.5	5556	AQ839814	AQ839814 260L13-C5
24	367.4	25.5	4087	BC024593	BC024593 Homo sapi

25	366.8	25.4	3143	3	HS8805999	BS537892 Homo sapi
26	366.6	25.4	839	1	AV700988	AV700988 AV700988
27	366.2	25.4	895	5	BU603620	BU603620 AGENCOURT
28	365.8	25.4	660	5	EX642324	EX642324 DKF2p686M
29	365.2	25.3	891	5	BU174155	BU174155 AGENCOURT
30	364.8	25.3	660	5	EX484570	EX484570 DKF2p686I
31	364.2	25.3	1654	3	CR591254	CR591254 full-length
32	364	25.2	671	4	BM722145	BM722145 UI-B-E00-
33	363.8	25.2	2044	3	BC037797	BC037797 Homo sapi
34	363.2	25.2	841	7	CF994276	CF994276 AGENCOURT
35	363	25.2	784	9	CL423322	CL423322 RP11-294J
36	361.4	25.1	611	5	BM996878	BM996878 UI-H-DHO-
37	360.8	25.0	820	5	BU852195	BU852195 AGENCOURT
38	360.8	25.0	930	5	BQ884038	BQ884038 AGENCOURT
39	360	25.0	1148	1	AV761207	AV761207 AV761207
40	359.8	25.0	667	9	AG150197	AG150197 Pan trogl
41	359.4	24.9	870	5	BQ711438	BQ711438 AGENCOURT
42	358.8	24.9	687	9	AG186062	AG186062 Pan trogl
43	357.8	24.8	679	2	BF346320	BF346320 602018525
44	357.6	24.8	888	5	BU594689	BU594689 AGENCOURT
45	357.4	24.8	722	8	AQ583981	AQ583981 RPC1-11-4

ALIGNMENTS

RESULT 1
CA437412
LOCUS
DEFINITION
CA437412
ACCESSION
CA437412
VERSION
CA437412.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 622)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 11-305, >ALU (matched complement) 221-440, >ALU (matched complement) 452-620, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..622
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-H-DT0-avk-a-06-0-UI"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP DT0"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP DT0 is a cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is

ACTGTCGCG.

TAG TISSUE=lung metastatic chondrosarcoma

TAG LIB=UI-H-DT0

TAG_SEQ=AACTGTCGCG"

ORIGIN

Query Match	36.2%	Score 521.8;	DB 6;	Length 622;
Best Local Similarity	95.9%;	Pred. No. 7.1e-17;		
Matches 590;	Conservative 0;	Mismatches 17;	Indels 8;	Gaps 5
QY	1	TTTTTTTTTTTGGAGATGGAGTTTTTCGGCTCTGTGTGCCAGCTGGAGTGCATATGGGCGCAA	60	
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QY	61	TCTCAGCTCACCGCAACCTCCGCGCTCCGGGGTTCAAGCGATTCTCTGCGCTCAGCCTCC	120	
Db	68	TCTCAGCTCACCGCAACCTCCGCGCTCCGGGGTTCAAGCGATTCTCTGCGCTCAGCCTCC	127	
QY	121	CAGTAGCTGGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTTTTTTTAA	180	
Db	128	TAGTAGCTGGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTTTTTTTAA	187	
QY	181	TAGAGATGGAGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGA	240	
Db	188	TAGAGATGGAGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGA	247	
QY	241	CCTCCGCTCTCGGCGTCCCAAAAGTGGT--AGATACAGGACTGGGCCACCATGCCCG	296	
Db	248	CTCCGCTCTCGGCGTCCCAAAAGTGGT--AGATACAGGACTGGGCCACCATGCCCGCGCT	307	
QY	297	TGCTCTGGCTAAATTTTTGTGTAGAAACAGGGTTTTCACTGATG-TGCCCAAGCTGGTCTCC	355	
Db	308	TGCTCTGGCTAAATTTTTGTGTAGAAACAGGGTTTTCACTGATGTTGCCAAGCTGGTCTCC	367	
QY	356	TGAGCTCAGCAGTCCACCTCGCTCAGCTCCCAAGTGTCTGGGATTACAGGGCT--GCA	413	
Db	368	TGAGCTCAGCAGTCCACCTCGCTCAGCTCCCAAGTGTCTGGGATTACAGGGGTGAGCG	427	
QY	414	GCGTGCCTGGCGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTTTACCCAG	473	
Db	428	ACGCTGCCTGGCGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTTTACCCAG	487	
QY	474	GATGAAGTGCAGTGGTGTGATCAGCTCACTGAGCGCTTCAACTCTCTGAGATCAAGC-A	532	
Db	488	GATGAAGTGCAGTGGTGTGATCAGCTCACTGAGCGCTTCAACTCTCTGAGATCAAGCAA	547	
QY	533	TCTCTCTGCTTCAGCTCCCAAGTAGCTGGGACCAAGACATGCACCACCTACACCTGGCT	592	
Db	548	TCTCTCTGCTTCAGCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGCT	607	
QY	593	AAATTTTATTTTAT	607	
Db	608	AAATTTTATTTTAT	622	

RESULT 2

Accession	Source	Organism
BC068461/c	Homo sapiens cDNA clone IMAGE:3034539, with apparent intron.	Human
LOCUS	3016 bp mRNA linear	HTC 19-JUL-2004
DEFINITION	Homo sapiens cDNA clone IMAGE:3034539, with apparent intron.	
ACCESSION	BC068461	
VERSION	BC068461.1	
KEYWORDS	GI:46249759	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	


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Db      8 TTTT...TTTGGAGTGGAGTTTTCGCTCTGTTGTCCTCCAGGCTGGAGTGCATGGCGCA 67
QY     61 TCTAGCTCAGCGCAACTCCGCTCCCGGGTCAAGCGATTCTCTGCTCAGCTCC 120
Db     68 TCTAGCTCAGCGCAACTCCGCTCCCGGGTCAAGCGATTCTCTGCTCAGCTCC 127
QY    121 CAGTACCTGGGATACAGCATGTGACCCAGGCTCGGCTAAATTTTGTATTTT 180
Db    128 TAGTACCTGGGATACAGCATGTGACCCAGGCTCGGCTAAATTTTGTATTTT 187
QY    181 TAGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
Db    188 TAGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTCGAACTCCCGACCTCAGATGATC 247
QY    241 CTCCTGCTCGGCTCCCAAGTGTCT--AGATACAGGACTGGCCACCATGCCCGG-CTC 296
Db    248 CTCCTGCTCGGCTCCCAAGTGTCTGAGATTACAGGCTGAGCCACCATGCCCGGCTC 307
QY    297 TGCCTGGCTAAATTTTGGTGAACAACAGGTTTCACTGATG-TGCCCAAGCTGGTCTCC 355
Db    308 TGCCTGGCTAAATTTTGGTGAACAACAGGTTTCACTGATGTTGCCCAAGCTGGTCTCC 367
QY    356 TGAGCTCAAGCAGTCCACTGCTCAGCTCCCAAGTGTGGGATTACAGGCGT--GCA 413
Db    368 TGAGCTCAAGCAGTCCACTGCTCAGCTCCCAAGTGTGGGATTACAGGCGTGGACC 427
QY    414 GCGTGGCTGGCTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 473
Db    428 ACCGTGGCTGGCTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 487
QY    474 GATGAAGTGCAGTGGTGTGATCACAGTCACTGCGAGCTTCAACT--CCTGAGATCAAGCA 532
Db    488 GATGAAGTGCAGTGGTGTGATCACAGTCACTGCGAGCTTCAACT--CCTGAGATCAAGCA 547

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RESULT 4
BC011119 1842 bp mRNA linear HTC 04-MAR-2003
LOCUS Homo sapiens, clone IMAGE:3047997, mRNA.
ACCESSION BC011119
VERSION BC011119.1 GI:15029795
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1842)
Strausberg, R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
cDNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAK Plate: 19 Row: 0 Column: 1
This clone has the following problem: retained intron.

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FEATURES
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        Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3047997"
                /tissue_type="Cervix, carcinoma"
                /clone_lib="NIH_MGC_12"
                /lab_host="DH10B"
                /note="vector: pCMV-SPORT6"

ORIGIN
    Query Match      27.5%; Score 396.2; DB 3; Length 1842;
    Besc Local Similarity 70.3%; Pred. No. 1.1e-48;
    Matches 746; Conservative 0; Mismatches 263; Indels 52; Gaps 14;

QY  2 TTTT...TTTTCAGATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGCGCAAT 61
Db  570 TTTT...TTTTCAGATGGAGTTCGGCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGTGAT 629
QY  62 CTCAGCTCAGCGCAACTCCGCTCCCGGGTCAAGCGATTCTCTGCTCAGCTCC 121
Db  630 CTCGCTTACTGCAAGCTCCGCTCCCGGGTTCACACCTTTCTCTGCTCAGCTCCCA 689
QY  122 AGTAGCTGGGATTACAGGCATGTGACCCAGCTGGTCTCGAACTCCCGACCTCAGATGATC 181
Db  690 AGTAGCTGGGACTACTGTGCGCCGACCAACGCGGCTAAATTTT-TTTCTATTTTGTAGT 748
QY  182 AGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTCGAACTCCCGACCTCAGATGATC 241
Db  749 AGAGACGGGGTTTTCACCGTGTAGCCAGATGGTCTTGATGTCTTGACCT--TGTGATTC 806
QY  242 CTCGCTCAGCGCTCCCAAGTGTAGATACAGGACTGGCCACCATGTCGCGGCTCTGCT 301
Db  807 ACCTGCTCGGCTCCCAAGTGTGGGATTACAGGAGTGGACCCAGCGCCGCGCTTGA 866
QY  302 GGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTG-GTCTCTGAGC 360
Db  867 TTTT...TTTAAATAGATGTTCTCATGTTGCCCGGACTAGTCTCAAACTCTCTGGGC 926
QY  361 TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGGATTACAG--GCGTGACCGCT 418
Db  927 TCAAGCCATCTCCACCTT-GGCTCCCAAGTGTCTGGGATTACAGTCTCAGCCACTGT 985
QY  419 GCCTGGCTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 478
Db  986 GCCTGGCTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1038
QY  479 AGTGAGTGGTGTGATCACAGTCACT-----GCAGCCTTCAAC 517
Db  1039 ACTGAGTGGTGGATCTCAGCTCACTGCAACCTCGGCTAGTTGAGCGCACTCTCGTC 1098
QY  518 TCCTGAGATCAAGC-ATCCTCTCTCAGCTCCCAAGTGTAGTGGGACCAAGACATGC 576
Db  1099 TCCTGGGTTCAAGCAATTTCTCTGCTCAGCTCCCGAGTGTAGATTACAGCGCAT 1158
QY  577 ACCACTACCTGGCTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 636
Db  1159 GCCACCACTGGCTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1215
QY  637 CTGTCAACCCAGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACTCTGCTCCCG 696
Db  1216 CTGTCA-CCAGCTGGAGTGCAGTGGCGCTGATCTTGGTCTCACTGCAACTCTGCTCCCG 1274
QY  697 GGTTCAGATTATTTCTCTGCGCCAGCTCTCTGAGTGTGGAGTGTACAGGCGCCACCCAC 756
Db  1275 GGTTCAGCCATTTCTCTG-GCCAGCTCTCAAGTGTGGAGTGTACAGGCGCCCGCCAC 1333
QY  757 GCCTAGCTAAAT-TTTTGTATTTTATTTAGTAGATGGG-TTCACCATGTTGCGCAGTT 814
Db  1334 CATGCCCGGCTAAATTTTGTATTTTATTTAGTAAGTGGGGTTTTCACCATGTTGGCAGGAT 1393
QY  815 GATCTTGATCTCTGGACCTTGTGATCTGCTGCTCGGCTCGGCTCCCAAGTGTGGGATTAC 874

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2

FEATURES

Location/Qualifiers


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1. 1345
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MDSB07"
/tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="MDS"
/notes="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"

ORIGIN
Query Match      26.6%; Score 383.6; DB 1; Length 1345;
Best Local Similarity 82.8%; Pred. No. 8.4e-47;
Matches 502; Conservative 0; Mismatches 86; Indels 18; Gaps 5;

QY 600 ATTATTTATTTTAAATTTTGTGACAGAGCTCAACTCTGTCAACCCAGGCTGAGTGCAG 659
Db 606 ATTTTNTNTNTTTTGTGACAGGAGTCTC-ACCTGTGCGCCAGGCTGAAGTGCAG 548
QY 660 TGGCGCAATCTTGCTCAGTCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCC 719
Db 547 TGGGGTCACTCAGTCACTGCAACCTCTGCTCCCGGGTTCAAGCAATCTCTGCCCTC 488
QY 720 AGCTCTCTAGTGTGGAGTCAAGCGC---CCACACGCTAGCTAATTTTGTGA 776
Db 487 AGCTCTCTAGTGTGGAGTCAAGCGC---CCACACGCTAGCTAATTTTGTGA 428
QY 777 TTTTGTAGATGGGTTTCCATGTTGCGCAGGTTGATCTTGTATCTTGACCTTGT 836
Db 427 TTTTGTAGATGACA-GGGTTTTCATGTTGCGCAGGCTTGTCTTGAACCTCTGACCTGT 369
QY 837 GATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGGCGTGAAGCACCACGCGCCG 896
Db 368 GATCCACCCACGAGTCTCTCAAGTGTGGGATTACAGGCGTGAAGCACCACGCGCG 309
QY 897 C-----TTATTTTAAATTTTGTGTTGTTGAAATCTCACTCTGTATCCC 945
Db 308 CTTCAATTTGCCATCTTTTTTTTTTTTTTTTTTTTCTTGAGATGGAGTCTCACTTATGGCC 249
QY 946 AGCTGGAGTGCATGGCCAAATCTGGCTCACTCAACCTCTGCTCCCGGCTCAAGC 1005
Db 248 AGCTGGAGTGTGTGGCAATCTCGGCTCACTGCAACCTCTGCTCCCGGATTCAAGT 189
QY 1006 GATTTCTCTGCTCAGCTCCCAAGCAGTGGGATTACGGGCACTGCCACACACCCCG 1065
Db 188 GATTTCTCTGCTCAGCTCCCGGATTACGGGATTACGGGCACTGCCACACACCCCG 129
QY 1066 CTAATTTTGTATTTTCAATPAGAGCGGGTTTTCACATATTTGTGAGGCTGTCTCAA 1125
Db 128 CTAATTTTGTATTTTCAATPAGAGCGGGTTTTCACATATTTGTGAGGCTGTCTCAA 69
QY 1126 CTCTGACCTCAGTGCACCTGCTGAGCTTCCAAAGTCTGGATTACAGCGTG 1185
Db 68 CTCTGACCTC--GTATCGCCCGCTCAGCTCCCAAGTCTGGATTACAGCGTG 11
QY 1186 AGCCAC 1191
Db 10 ACCAC 5

RESULT 8
BQ722917/c
LOCUS
DEFINITION
AGENCOURT_8100507 Lupeki_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6190443 5', mRNA sequence.
BQ722917
VERSION
BQ722917.1 GI:21861803
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
1 (bases 1 to 910)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLES
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
cdna library prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13589 row: e column: 04
High quality sequence stop: 653.
Location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190443"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupeki_sympathetic trunk"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCCG-3' and
5'-GACTAGTCTAGTCGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupeki, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN
Query Match      26.3%; Score 379; DB 5; Length 910;
Best Local Similarity 80.8%; Pred. No. 4.5e-46;
Matches 514; Conservative 0; Mismatches 91; Indels 31; Gaps 5;

QY 595 TTTTATTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAG 654
Db 643 TTTTATTTTATTTTATTTTGTGAGCGGAGTCT-TGCTCTGTGCGCCAGGCTGGAG 595
QY 655 TGCAGTGGCGCAATCTTGCTCAGTCAACCTCTGCTCCCGGGTTCAAGTTATTCTCT 714
Db 584 TGCAGTGGCGCAATCTTGCTCAGTCAACCTCTGCTCCCGGGTTCAAGCGATTCTCT 525
QY 715 GCCCGAGCTCTGAGTAGCTGGGACTACAGGCG---CCACACGCTAGCTAATTTT 771
Db 524 GCTCAGCTCTCTGAGTAGCTGGGACTACAGGCAATGCCACGCTCGGCTAATTTT 465
QY 772 TTGTATTTTGTAGAGATGGGGTTTCCCATGTTGCGCAGGTTGATCTTGTATCTCTG 831
Db 464 TGTATTTTATGGAGACAGGGTTTCCACGCTGTAGCCAGGATGGTCTCGATCTCTGAT 405
QY 832 CTTGTGATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGCGTGAAGCCACG 891
Db 404 CTTGTGATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGCGTGAAGCCACGCG 345
QY 892 CCGGCG-----TTATTTTAAATTTTGTGTTTGTGAATCG 927
Db 344 CCGGCGCTTCCCTAGTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGACGCG 285
QY 928 AATCTCACTCTGTATACCCAGGCTGGAGTGCATATGGCCAAATCTCGGCTCACTGCAACCTC 987
Db 284 AGTCTGCTCTGTGCGCCAGGCTGGAGTGCATGCGGGGATCTCGGCTCACTGCAAGCTC 225
QY 988 TGCCTCCCGGGCTCAAGCGATTCTCTGTCTCAGCTCCCAAGCAGCTGGGATTACGGGC 1047
Db 224 TGCCTTCCGGGTTCCAGCGCATTTCTCTGCTCAGGCTCCCAAGTAGCTAGCTAGGACTACAGGC 165

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QY 1048 ACCTGCCACACACCGCGCTAA-TTTTGTATTTTCAATAGAGCGGGTTTCCACATAT 1106
Db 164 GCCCGCCATAGCCCGGCTAAATTTTTTGTATTTTGTAGTAGAGACGGGGTTTCCACCGTTT 105
QY 1107 TTGTCAAGGTGTCTCAAACTCTGACCTCAGGTGACCCACCTGCTCAGCCCTCCAAAG 1166
Db 104 TAGCCGGGATGTCTCGATCTCTGACCTC--GTGATCGCCCGCTCGGCCCTCCAAAG 47
QY 1167 TGCTGGGATTACAGCGGTGAGCCACTCACCAGCC 1202
Db 46 TGCTGGGATTACAGCGGTGAGCCACCGCGCCCGCC 11

RESULT 9
AV700498
LOCUS AV700498 GKC Homo sapiens cDNA clone GKCAAC05 3', mRNA linear EST 16-JAN-2002
DEFINITION AV700498
ACCESSION AV700498
VERSION AV700498.1 GI:10302469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 767)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PubMed 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCAAC05"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 26.2%; Score 378.4; DB 1; Length 767;
Best Local Similarity 83.1%; Pred. NO. 5.9e-46;
Matches 481; Conservative 0; Mismatches 87; Indels 11; Gaps 4;

QY 635 CTCTGTCAACCGGTGGAGTGCAGTGGCGAATCTTGGCTCACTGCACCTTCGCTCC 594
Db 13 CTCTGTCAACCGGTGGAGTGCAGTGGCGAATCTTGGCTCACTGCACCTTCGCTCC 72
QY 695 CGGGTTCAAGTTATTTCTCTCGCCCGCCAGCCCTCTGAGTAGCTGGGACTACAGCGC---CCC 751
Db 73 CGGGTTCAACCGGTATTTCTCTCGCTCAACCTCCCGAGTAGCTGTGAATACAGCGCTCCGCC 132
QY 752 ACCAGCGCTAGCTAAATTTTTTTGTATTTTGTATTTTGTAGAGATGGGG-TTCACCATGTTCGCCA 810
Db 133 ACCAGCGCGCACTAAATTTTTTTGTATTTTGTATTTTGTAGAGACGGGGTTTACCGGTGTAGCCA 192

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QY 811 GGTTCATCTTGTATCTCTGAGACTTGTGATCTGCCTTGCCTCGGCTCCCAAGTGTGGGA 870
Db 193 GGATGGTCTGGATCTCTGAGACTTGTGATCTGCCTTGCCTCGGCTCCCAAGTGTGGGA 252
QY 871 TTACAGGCGTGAAGCCACACCGCGGCTTATTTTAAATTTTGTGTTGTTGAAATGGAAT 930
Db 253 TTACAGGCTTGAAGCCACCGCGGCTCT-----TATTTTTTTTGTAGATGGAGT 306
QY 931 CTCACCTGTATCCAGGCTGGAGTGCAAATGGCCAAATCTCGGCTCACTGCACACCTCTGC 990
Db 307 CTCACACTGTCACTGGGCTGGAGTGCAGTGGAGCGATCTCGGCTCACTGCACACCTCCGC 366
QY 991 CTCGCGGCTCAAGCGATCTCTGTCTCAGGCTCCCAAGCAGCTGGGATTAAGGCGACC 1050
Db 367 CTCCTGGGTTCAAGAGATTTCTCTGCTCAGCCTCCCAAGTAGCTGGGATTAAGGCTGCC 426
QY 1051 TGCCACCAACACCCCGCTA-ATTTTGTATTTTCAATAGAGCGGGTTTCCACATATTG 1109
Db 427 CACCAACAGCTGGCTAGTTTGTATTTTGTATTTTGTAAAGATGGGTTTCCACATGCTGG 486
QY 1110 TAGGCTGGTCTCAAACTCTGACCTCAGGTGAGCCACCTGCTCAGCCTTCCAAAGTGC 1169
Db 487 CCAGGCTGGTCTTGAATCTCTGACATCAGGTGATCCGNCACCTTAGCCCTCCCAAGTGC 546
QY 1170 TGGGATTACAGCGGTGAGCCACCTCACCAGCGCGCTAA 1208
Db 547 TTGGATTACAGCGGTGAGCCACCTACCTGGCCAGCAAA 585

RESULT 10
CD709038
LOCUS CD709038/c
DEFINITION EST25565 human nasopharynx Homo sapiens cdna, mRNA linear EST 25-JUN-2003
ACCESSION CD709038
VERSION CD709038.1 GI:32239668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 613)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cdna
library from southern Chinese"

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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cdna
library from southern Chinese"

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Query Match 26.2%; Score 377.6; DB 6; Length 613;
Best Local Similarity 83.0%; Pred. NO. 8.4e-46;
Matches 483; Conservative 0; Mismatches 84; Indels 15; Gaps 4;

QY 634 ACTCTGTCAACCGGTGGAGTGCAGTGGCGAATCTTGGCTCACTGCACCTTCGCTCC 693
Db 610 ACTCTGTCCGCGGCTGGAGTGCAGTGGCGGTGATCTCAGCTCACTGCACACCTTCGCTC 551
QY 694 CCGGGTTCAAGTTATTTCTCTCGCCCGCCAGCCTCTCTGAGTAGCTGGGACTACAGGCGCCAC 753

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Db 550 CTGGGTTCAAGCAATCTCTCTGCTCAGCTCTCTGAGTAGCTGGGACTACAGCGCGCCG 491
QY 754 CAGGCTAGCTAAT-TTTTTTGTATTTTAGTAGAGA-TGGGGTTCACCATGTTCGCCAG 811
Db 490 CACCAGCCCGCAATATTTTGTATTTTAGTAGAGACAGGGTTTCATCATGTGGCCAG 431
QY 812 GTTGATCTTGATCTCTGGACCTTGATCTGCTGCTCGGCTCCCAAAGTCTGGGAT 871
Db 430 GCTTGTCTTGAATCTCTGACCTCGTGATCCACCCACCGACTCTCAAGTCTGGGAT 371
QY 872 TACAGCGGTGAGCCACACCGCGGC-----TTATTTTAAATTTTGTGTTT 920
Db 370 TACCGCGGTGAGCCACCATGCGCGGCTCATTTGGCCAATCTTTTTTTTTTCTTT 311
QY 921 GAAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCAATGGCCAAATCTCGGCTCACATG 980
Db 310 GAGATGGAGTCTCACTCTATTTGCCAGGCTGGAGTCTGGACAAATCTCGGCTCACATG 251
QY 981 CAACTCTGCTCTCGGCTCAAGCGATTTCTCTGTCTCAGGCTCCCAAAGCTGGGAT 1040
Db 250 CAACTCTGCTCTCGGATTCAGTGATTTCTCTGCTCAGGCTTCGGAGTAGCTGGGAT 191
QY 1041 TACGGCACCTGCCACACACCGGCTAATTTTGTATTTTCAATTAGAGCGGGTTTCA 1100
Db 190 TACAGGCATGCCACCATGCGGAGCTAATTTTGTATTTTACTAGAGACAGGGTTTCA 131
QY 1101 CCATATTTCTAGGCTGGTCTCAAACTCTGACCTCAGGTGACCCACCTGCTCAGGCTT 1160
Db 130 CCATATTTGTAGGCTGGTCTCAAACTCTGACCTC--GTGATCGCGCGCTCAGGCTC 73
QY 1161 CCAAGTGTGGGATTTACAGGCGTGAGCCACCTCACCCAGCC 1202
Db 72 CCAAGTGTGGGATTTACAGGCGTGAACCACTGCGCGCGGCC 31

RESULT 11
LOCUS CR614786
DEFINITION full-length cDNA clone CS0DF06YD23 of Fetal brain of Homo sapiens (human).
ACCESSION CR614786
VERSION CR614786.1 GI:50495593
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
Redwood City, CA 94063
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .2097
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF06YD23"
/tissue_type="Fetal brain"

FEATURES

RESULT 12
LOCUS CR614786
DEFINITION full-length cDNA clone CS0DF06YD23 of Fetal brain of Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
Redwood City, CA 94063
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .2097
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF06YD23"
/tissue_type="Fetal brain"

ORIGIN
Query Match 26.2%; Score 377.6; DB 3; Length 2097;
Best Local Similarity 71.6%; Pred. No. 5.4e-46;
Matches 614; Conservative 0; Mismatches 219; Indels 25; Gaps 8;
/plasmid="pCMVSPORT_6"
QY 352 CTCCTGAGCTCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGGATTCAGGCG-- 409
Db 480 CTCCTGGGTTCAAGCTATTCTCTGCTCAGCTTCTGAGTAGCTGGGATTTAGGCGCA 539
QY 410 TCGACCGTCTGCTGCTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 469
Db 540 TGCCACCATGCTGCTGCTAATTTTGTATTTTATTTTATTTTATTTTATTTTATTTT 599
QY 470 CCAGGATGAAGTGCAGTGTGTGATCAGACCTCAGTGCAGCTTCAATGATCCACCTGCT 529
Db 600 CAGGCTGGTCTTGAATCTCTGACCTCAATGATCCACCTGCTGCTTCTCTCCCGAAGCG 659
QY 530 GCATCTCTGCTCAGCTCCCAAGTGTCTGAGTGTGGGACCAAGACATGACCACTACAC 589
Db 660 GGGATTAGAGGTATGAGCCACCATGCGCGAGGTCTCTCTCTTTTAAACTTTC----- 712
QY 590 GCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 649
Db 713 -----TTTAAATTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 765
QY 650 TGGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAGGTTAT 709
Db 766 TGGAGTGCAGTGGTGCATCTTGGCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 825
QY 710 CTCCTGCGCCAGCTCTGAGTAGTGTGGGACTACAGGCGCCCAACGCTAGCTAAT-T 768
Db 826 CTCCTGCGCTCAGCTCTGAGTAGTGTGGGATTTAGAGGACACCCACCAAGCGCCACCT 885
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Db 886 TTTTGTATTTTGTAGTAGAGACAGGGTTTACCATGTTTGGACAGGCTGTCTTGAACGCC 945
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Db 946 TGACCTCAGGTTGATTCACCCCGGCTCCCAAGTGTCTGGGATTTACAGGCGTGAGCC 1005
QY 886 ACCACGCGCGCTTATTTTAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 945
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Db 1302 GAACCCATGCCCAGCC 1319

FEATURES

RESULT 12
LOCUS CR614786
DEFINITION full-length cDNA clone CS0DF06YD23 of Fetal brain of Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
Redwood City, CA 94063
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. .2097
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/mol_type="mRNA"
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/clone="CS0DF06YD23"
/tissue_type="Fetal brain"

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Qy	900	ATTTTAATTTTTTTTGTGTTGAAAATGGAATCTCACTCTGTTACCAGGCTCGAGTCGACCA	959
Db	298	-----CTTTTTTTTTTTTGTGAGACAGAGTCTCGCTCAGTTGCCCCAGGCTCGAGTCGAC	348
Qy	960	TGGCCCAAATCTCGGCTCACCTGCAACCTCTGCGCTCCCGGCTCAAGCGATTCTCTGTCTC	101
Db	349	TGGCGTGATTTTCACTGCTCCTGCAATCTCCACCTCCCAAGTTCACGCAATTTCTCTGCTC	408
Qy	1020	AGCTTCCAAGCAGCTGGGATTAAGGGGACCTGCGCCACACACACCCCGCTAATTTTGTATT	107
Db	409	AACCTCCGAGTAGTTGAGACTACAGGCCCCCGCCACACACCCAGCTGAATTTTTTTTT	468
Qy	1080	TTCAATTAGAGCGGGGTTTCAACCATATTTGTGAGGCTGCTCTCAAACTCCTGACCTCAGG	113
Db	469	TTTAGTAGAGACAGGGTTTCAACCATATTTGCGCAGGCTAGTCTTGAACCTCTGACCTCAG	528
Qy	1140	TGACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAAGGCGTGGAGCCACTCACCCA	119
Db	529	TGATCCACCTGCTCGGCTCCCAAGTGTGAGATTACAGGTGTGAGCCATGGCGGCTG	588
Qy	1200	GCCGGCT 1206	
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RESULT 13			
LOCUS	CD690152	628 bp mRNA linear EST 25-JUN-2000	
DEFINITION	EST6875 human nasopharynx Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD690152		
VERSION	CD690152.1	GI:32210629	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 628)	Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Liu, X.-Q., Zhou, Y.,	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn.		
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		/clone_lib="human nasopharynx"	
		/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"	
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Db	625	TTTTTTTGGAGCAGAGTCTCACTCTGTCGCCCAAGGCTGGAGTGCAGTGCAGTGCAGT	566
Qy	674	CTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTCTCTGCCCCCAGGCTCTCTGAGTAG	733

Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp547l147) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp547l147>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

1. .2777
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/clone="DKFZp547l147"
/tissue_type="brain"
/clone_lib="547 (synonym: hfbri). Vector pSport1; host
DH10B; sites NotI + Sali"
/dev_stage="fetal"
/note="genomic"

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Best Local Similarity 71.3%; Pred. No. 1e-45;
Matches 581; Conservative 0; Mismatches 221; Indels 13; Gaps 6;
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QY 665 CAATCTTGGCTCAGTGCACCTCTGCTCCGGGTTCAGTTATCTCTGCTGCCAGGCT 724
Db 2718 CAATCTTGGCTCAGTGCACCTCTGCTCCGGGTTCAGTTATCTCTGCTGCCAGGCT 2659
QY 725 CTTGATAGTCTGGGACTACAGGC--GCCACACAGGCTAGCTAAATTTTGTATTTT 781
Db 2658 CCGAATAGTCTGGGACTATAGGACTATGCGATGCGCCAGCTAATTTTGTATTTTAG 2599
QY 782 AGTAGAGATGGGTTTCCAGTGTTCGCGAGGTGATCTTGTATCTCTGGACCTTTGTGATCT 841
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QY 902 TTTTAAATTTTGTGTTGTTGAAATGGAATCTCACTCTGTACCCAGGCTGGAGTGCAGATG 961
Db 2481 TCTTATTTATTTATTTTGTAGGTGGAGTCTCACTCTGCTCAGGCTGGTGTGCAATG 2422
QY 962 GCCAAATCTCGGCTCACTGCAACCTTGTGCTCCCGGGTCAAGCGATTCTCTGTCTCAG 1021
Db 2421 ATGCAATCTGGCTCACTGCGCCTCTGCTCTCAGGTTCAACCAATCTCTCTGTCTCAG 2362
QY 1022 CTTCCCAAGCAGTGGGATTACGGGACCTGCGCACCAACCCCGCTAATTTTT--GTATT 1079
Db 2361 CTTCTCTAGTAGTCTGAGATTACGGGATGTGCCATGACGCTGGGCTAATTTTGGTATT 2302
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QY 1200 GCCGGCTAAATTTAGATAAAAAAATATGTAGCA----ATGGGGGCTTTGCTATGTTGCC 1255
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QY 1376 CATGTCAAACTGCAAAATTCAGTAGTAACAGAGTT 1410
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Search completed: September 15, 2005, 21:58:53
Job time : 5124 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 14:42:12 ; Search time 6434 Seconds
(without alignments)
10859.873 Million cell updates/sec

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Sequence: 1 TTTT...TTTGGAGGAG.....TTAAACAAGCTTTAGACA 1442

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Gapop 10_0 , Gapext 1.0
Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg.*
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5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1442	100.0	1442	6	AR072690 Sequence
3	1442	100.0	1442	6	AR073235 Sequence
4	1442	100.0	1442	6	AX594290 Sequence
5	1442	100.0	1442	6	AX599994 Sequence
6	1442	100.0	1442	6	AX709024 Sequence
7	1442	100.0	1442	6	AX709356 Sequence
8	1442	100.0	1442	6	AX770807 Sequence
9	1442	100.0	1442	6	AX774635 Sequence
10	1442	100.0	1442	6	BD070526 Transgeni
11	1442	100.0	1442	9	AF010144 Homo sapi
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14	1080.2	74.9	1381	6	AR051479 Transgeni
15	1080.2	74.9	1381	6	AR072619 Sequence
16	1080.2	74.9	1381	6	AR073164 Sequence
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26	587.8	40.8	148525	2	AC016675	AC016675 Homo sapi
27	578.4	40.1	121272	2	AC004956	AC004956 Homo sapi
28	573.6	39.8	186161	2	AC151887	AC151887 Saimiri s
29	567.6	39.4	170630	2	AC016905	AC016905 Homo sapi
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33	559.2	38.8	110459	9	AC117378	AC117378 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AR051550 1442 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 120 from patent US 5830670.
ACCESSION AR051550
VERSION AR051550.1 GI:5974914
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1442)
AUTHORS de la Monte, S. and Wands, J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 120 03-NOV-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
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RESULT 2
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LOCUS AR072690 1442 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 120 from patent US 5948634.
ACCESSION AR072690
VERSION AR072690.1 GI:9999454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1442)
AUTHORS de la Monte, S. and Wands, J. R.
TITLE Neural thread protein gene expression and detection of alzheimer's disease
JOURNAL Patent: US 5948634-A 120 07-SEP-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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Sequence 120 from patent US 5948888.
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VERSION
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Unclassified.
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de la Monte, S. and Wands, J. R.
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Patent: US 5948888-A 120 07-SBP-1999;
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DEFINITION Sequence 1 from Patent WO02074323.
ACCESSION AX594290
VERSION AX594290.1 GI:28375449
KEYWORDS
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ORGANISM Homo sapiens
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REFERENCE 1
Auerback, P.
AUTHORS
TITLE Methods of using neural thread proteins to treat tumors and other
conditions requiring the removal or destruction of cells
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AVERBACK, Paul (CA)
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 Nymox Pharmaceuticals Corporation (CA)
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 ACCESSION AX709024
 VERSION AX709024.1 GI:29564697
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 Averbach, P.A.
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 KEYWORDS
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 METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF NEURAL THREAD
 PROTEINS
 JOURNAL Patent: WO 02092115-A 1 21-NOV-2002;
 NIMOX CORPORATION (CA)
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ACCESSION BD070526
VERSION BD070526.1 GI:22616129
KEYWORDS JP 2001513777-A/1.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 1442)
AUTHORS Monte,S.D. and Wands,J.R.
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 AUTHORS Monte,S.M., Ghanbari,K., Frey,W.H., Beheshti,I., Averbach,P.,
 Hauser,S.L., Ghanbari,H.A. and Wands,J.R.
 TITLE Characterization of the AD7c-NTP cDNA expression in Alzheimer's
 disease and measurement of a 41-kD protein in cerebrospinal fluid
 J. Clin. Invest. 100 (12), 3093-3104 (1997)
 JOURNAL 98064067
 MEDLINE 9399956
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 REFERENCE De la Monte,S.M. and Wands,J.R.
 AUTHORS Direct Submission
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 Hospital, 149 13th Street, Room 7308, Charlestown, MA 02129, USA
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hydroxymethylglutaryl-CoA lyase, GALE (UDP-galactose-4-epimerase)
ESTs, GSS, STS, CpG island, complete sequence.
ACCESSION
AL031295
VERSION
AL031295.1 GI:4376011
KEYWORDS
HTG; elongin A; GALE; HMGCL; hydroxymethylglutaryl-CoA lyase; RNA
polymerase II elongation factor.
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 124001)
Direct Submission
Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 7, 1999 this sequence version replaced gi:4056542.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP5-886K2 is from the library RPCI-5 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
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Db 4649 GTATCAG 4643

RESULT 13
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LOCUS
DEFINITION
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Transgenic animals and cell lines for screening drugs effective for
the treatment or prevention of Alzheimer's disease.
ACCESSION
BD070528.1 GI:22616131
VERSION
JP 2001513777-A/3.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1418)
Monte,S.D. and Wands,J.R.
AUTHORS
Transgenic animals and cell lines for screening drugs effective for
the treatment or prevention of Alzheimer's disease
TITLE
Patent: JP 2001513777-A 3 04-SEP-2001;
JOURNAL
THE GENERAL HOSPITAL CORP
COMMENT
OS Unidentified
PN JP 2001513777-A/3
PD 04-SEP-2001
PF 26-FEB-1998 JP 1998537813
PR 26-FEB-1997 US 60/038908
PI SUZANNE DELA MONTE,JACK R WANDS
PC C07H21/02,C07H21/04,C12N5/00,C12N15/00,C12O1/02,A61K48/00, PC
A61K49/00
CC Strandedness: Both;
CC Topology: Both;
CC Transgenic animals and cell lines for screening drugs CC
CC effective for the
treatment or prevention of Alzheimer's disease FH Key
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ACCESSION	AR072619				
VERSION	AR072619.1	GI:99999383			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1381)				
TITLE	de la Monte,S. and Wands,J.R.				
JOURNAL	Neural thread protein gene expression and detection of alzheimer's				
FEATURES	disease				
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Job time : 6446 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 14:22:52 ; Search time 942 Seconds
(without alignments)
10138.084 Million cell updates/sec

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Perfect score: 1442
Sequence: 1 TTTTTCCTTTTGGATGGAG.....TTAAACAAGCTTTAGACA 1442

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1442	100.0	1442	8	Abx08221 DNA encod
5	1442	100.0	1442	8	Abz23236 Nucleotid
6	1442	100.0	1442	8	Aal54224 AD7C-neur
7	1442	100.0	1442	10	Adb37519 Human neu
8	1442	100.0	1442	13	Acc84453 AD7C-NTP
9	1223.4	84.8	1418	2	Adr14408 Human NP-
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11	1077	74.7	1381	2	Aat27765 AD 10-7 h
12	590.4	40.9	33112	10	ACC85730
13	587.8	40.8	65608	6	ABL62910
14	587.8	40.8	65608	6	ABL64414
15	587.8	40.8	65608	6	ABL67668
16	535.2	37.1	79528	6	Aal50814 Human can
17	535.2	37.1	79528	12	Adq19802 Human sof
18	524.4	36.4	62944	6	ABL68262 Kidney ca
19	524.4	36.4	62944	6	ABL66947 Lung canc
20	517.2	35.9	33747	4	Aak73093 Human imm

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c	23	513.4	35.6	43545	6	ABK85018	Human cad
c	24	513	35.6	21470	4	ABK42270	Genomic s
c	25	513	35.6	21470	9	ABK60426	Connectiv
c	26	511.6	35.5	5262	4	AAK71768	Human imm
c	27	511.6	35.5	5262	4	AAK71769	Human imm
c	28	511.4	35.5	60729	12	ADQ97864	Human can
c	29	502.8	34.9	75252	11	ACN44450	Human can
c	30	501.4	34.8	3446	13	ADR07063	Full leng
c	31	496.4	34.4	115756	8	ACD13448	Human DNA
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c	34	490.2	34.0	130001	12	ADJ96282	Human bre
c	35	490	34.0	51837	13	ABD33453	Human can
c	36	489.6	34.0	76201	12	ADJ62814	Human can
c	37	489.6	34.0	24167	5	ABR16132	Human ner
c	38	489.6	34.0	59999	13	ADR28249	Human low
c	39	482.8	33.5	276276	11	ACN44350	Human gen
c	40	482.8	33.5	60815	11	ACN43882	Human gen
c	41	482.6	33.5	22235	13	ABD33054	Human can
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c	44	479.6	33.3	44820	6	AAI19703	Reference
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ALIGNMENTS

RESULT 1
ABN89470
ID ABN89470 standard; DNA; 1442 BP.
XX
AC ABN89470;
XX

DT 02-SEP-2002 (first entry)

DB Neural thread protein (NTP) encoding nucleotide sequence.

XX Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;

KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;

KW hypoxia; ischaemia; cerebral infarction; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 15..1142

FT FT /*tag= a

FT FT /product= "Neural thread protein"

XX WO200234915-A2.

XX PD 02-MAY-2002.

XX PF 25-OCT-2001; 2001WO-US042813.

XX PR 27-OCT-2000; 2000US-00697590.

XX (NYMO-) NYMOX PHARM CORP.

XX PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;

XX DR WPI; 2002-507998/54.

XX DR P-PSDB; ABB81538.

XX New Harlil peptide sequences of the Neural Thread protein, useful in
PT therapeutic assays, e.g. as targets for developing drugs for treating
PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
PT these diseases.

XX Example 1; Fig 1; 53pp; English.

CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81529 to ABB81529 and
 CC their homologues, which are referred collectively as Harilil peptides (1).
 CC (1) have neuroprotective, nootropic, vasotropic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Harilil peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Harilil
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Harilil peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases. The present sequence encodes a neural thread protein
 CC given in the exemplification of the present invention
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Query Match 100.0%; Score 1442; DB 6; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 CTCTCGTCTCGGCTCCCAAGTGTCTAGATACAGGACTGGCCACCAATGCCGGCTCTGCC 300
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QY 1441 CA 1442
 DB 1441 CA 1442

RESULT 2
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 ID AAD46671 standard; DNA; 1442 BP.
 XX
 AC AAD46671;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DB AD7c-NTP gene.
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 KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
 KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
 KW inflammatory disease; nutritional deficiency disease; genetic disease;
 KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
 KW infectious disease; congenital malformation; enzyme deficiency disease;
 KW amyloid disease; fibrosis disease; storage disease; radiation disease;
 KW poisoning; environmental disease; endocrine disease; protein therapy;
 KW degenerative disease; mechanical disease; AD7c-NTP protein; gene; ds.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
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 FT /product= "AD7c-NTP protein"
 PN WC200274323-A2.
 XX 26-SEP-2002.
 PD 08-MAR-2002; 2002WO-1B001959.
 XX 08-MAR-2001; 2001US-0273957P.
 XX (AVER/) AVERBACK P.
 XX AVerback P;
 XX WPI: 2002-759864/82.
 XX P-PSDB; AAE29142.
 XX
 XX Treating a condition in a patient requiring removal or destruction of
 XX cells, such as a benign or malignant tumor of a tissue or an inflammatory
 XX disease, comprises administering a neural thread protein (NTP) or a NTP
 XX gene to a mammal.
 XX
 XX Example 2; Fig 1; 70pp; English.
 XX
 XX The invention relates to a method for treating a condition in a patient
 XX requiring removal or destruction of cells. The method involves
 XX administering to a mammal a neural thread protein (NTP), or administering
 XX to a tumour or other target cell a NTP gene, where the expression of the
 XX NTP gene is induced resulting in expression of the NTP protein. The
 XX method and NTP are useful for treating a condition in a patient requiring
 XX removal or destruction of cells, such as a benign or malignant tumour of
 XX a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
 XX preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
 XX bacterially, or parasitically altered tissue, or a malformation of a
 XX tissue. Other conditions include a cosmetic modification to a tissue,
 XX such as removal of unwanted facial hair, warts or unwanted fatty tissue,
 XX a vascular disease, particularly atherosclerosis or arteriosclerosis,
 XX haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
 XX disease, metabolic disease, hereditary/genetic disease, traumatic disease
 XX or physical injury, nutritional deficiency disease, infectious disease,
 XX congenital malformation, amyloid disease, fibrosis disease, storage
 XX disease, enzyme deficiency disease, poisoning, intoxication, degenerative
 XX disease, radiation disease, environmental disease, endocrine disease or
 XX mechanical disease. The invention is useful in protein therapy and gene
 XX therapy. The present sequence is AD7c-NTP gene
 XX
 XX Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 1442; DB 6; Length 1442;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTATTTTGGAGTGGAGTTTCCTCTTGTGCTCCAGGCTGGAGTGAATGGCGCAA 60
 Db 1 TTTTATTTTGGAGTGGAGTTTCCTCTTGTGCTCCAGGCTGGAGTGAATGGCGCAA 60
 QY 61 TCTCAGCTCAGCGCAACCTCCGGCTCCGGGTTCAAGCGATTCCTCTGCTCAGCCTCCC 120
 Db 61 TCTCAGCTCAGCGCAACCTCCGGCTCCGGGTTCAAGCGATTCCTCTGCTCAGCCTCCC 120
 QY 121 CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTGTAG 180
 Db 121 CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTGTAG 180
 QY 181 TAGAGATGGAGTTTCTCCATTTTGTGTGAGTGGTCTCGAATCTCCGACCTCAGATGATC 240
 Db 181 TAGAGATGGAGTTTCTCCATTTTGTGTGAGTGGTCTCGAATCTCCGACCTCAGATGATC 240
 QY 241 CCTCGCTCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCAATGCCCGGCTCTGCC 300
 Db 241 CCTCGCTCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCAATGCCCGGCTCTGCC 300

QY 301 TGGCTAAATTTTGTGTGAGAAAACAGGGTTTCACTGATGTGCCAAGCTGTCTCTCTGAGC 360
 Db 301 TGGCTAAATTTTGTGTGAGAAAACAGGGTTTCACTGATGTGCCAAGCTGTCTCTCTGAGC 360
 QY 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAAGTGTGGGATTAACAGGCGTGCAGCGTGC 420
 Db 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAAGTGTGGGATTAACAGGCGTGCAGCGTGC 420
 QY 421 CTGGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
 Db 421 CTGGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
 QY 481 TGCAGTGTGTGATCACAGCTCACTGACGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
 Db 481 TGCAGTGTGTGATCACAGCTCACTGACGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
 QY 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGAATGACCACTACACCTCGGCTAAATTTTAA 600
 Db 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGAATGACCACTACACCTCGGCTAAATTTTAA 600
 QY 601 TTTTATTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGCTGCAGT 660
 Db 601 TTTTATTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGCTGCAGT 660
 QY 661 GGGCGAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTTATTTCTCTGCCCCA 720
 Db 661 GGGCGAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTTATTTCTCTGCCCCA 720
 QY 721 GCCTCTCAGTAGCTGGGACTACAGCGGCCCAACAGCTAGCTAAATTTTGTATTTT 780
 Db 721 GCCTCTCAGTAGCTGGGACTACAGCGGCCCAACAGCTAGCTAAATTTTGTATTTT 780
 QY 781 TAGTAGAGATGGGGTTTCAACATGTTTGCAGAGTTGATCTTGATCTCTGACCTTGTGATC 840
 Db 781 TAGTAGAGATGGGGTTTCAACATGTTTGCAGAGTTGATCTTGATCTCTGACCTTGTGATC 840
 QY 841 TGCTGCTCTCGGCTCCCAAAGTGTGGGATTAACAGGCTGAGCCACCAACCGCGCTTA 900
 Db 841 TGCTGCTCTCGGCTCCCAAAGTGTGGGATTAACAGGCTGAGCCACCAACCGCGCTTA 900
 QY 901 TTTTAAATTTTGTGTTGTTGAAATGGAATCTCACTCTGTATACCAGGCTGGAGTGCAAT 960
 Db 901 TTTTAAATTTTGTGTTGTTGAAATGGAATCTCACTCTGTATACCAGGCTGGAGTGCAAT 960
 QY 961 GSCCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCCTCTCTCA 1020
 Db 961 GSCCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCCTCTCTCA 1020
 QY 1021 GCCTCCCAAGCAGCTGGGATTAACGGGCACCTGSCCACCACACCCCGCTAAATTTTGTATTT 1080
 Db 1021 GCCTCCCAAGCAGCTGGGATTAACGGGCACCTGSCCACCACACCCCGCTAAATTTTGTATTT 1080
 QY 1081 TCATTAGAGGCGGGTTTCAACATATTTGTGAGGCTGTCTCAAACTCTCTGACCTCAGGT 1140
 Db 1081 TCATTAGAGGCGGGTTTCAACATATTTGTGAGGCTGTCTCAAACTCTCTGACCTCAGGT 1140
 QY 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAACAGGCTGAGCCACCTCACCAG 1200
 Db 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAACAGGCTGAGCCACCTCACCAG 1200
 QY 1201 CCGGCTAAATTTAGATAAAAAAATATGTAGCAATGGGGGCTTTGCTATGTGSCCAGGCT 1260
 Db 1201 CCGGCTAAATTTAGATAAAAAAATATGTAGCAATGGGGGCTTTGCTATGTGSCCAGGCT 1260
 QY 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCAGTCA 1320
 Db 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCAGTCA 1320
 QY 1321 CATTTTTTAAACAGTTACATCTTTATTTTATTTAGTATAGTAAGTAATTAACAATGATGT 1380
 Db 1321 CATTTTTTAAACAGTTACATCTTTATTTTATTTAGTATAGTAAGTAATTAACAATGATGT 1380

841 TGCCCTGCTCGGCTCCCAAGTGTGGGATACAGCGGTGAGCCACCGCCGCTTA 900
 901 TTTTAAATTTTGTGTTGTAATGTAATCTCACTCTGTGTACCGAGGCTGGAGTCAAT 960
 901 TTTTAAATTTTGTGTTGTAATGTAATCTCACTCTGTGTACCGAGGCTGGAGTCAAT 960
 961 GGCCAAATCTGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTTCTCTGTCTCA 1020
 961 GGCCAAATCTGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTTCTCTGTCTCA 1020
 1021 GCCTCCCAAGCAGCTGGGATACGGGCACTGCGCCACACACCCCGCTAAATTTTGTATTT 1080
 1021 GCCTCCCAAGCAGCTGGGATACGGGCACTGCGCCACACACCCCGCTAAATTTTGTATTT 1080
 1081 TCATTAGAGCGGGGTTTCAACATATTTGTGAGGCTGTCTCAAACTCTGACCTCAGGT 1140
 1081 TCATTAGAGCGGGGTTTCAACATATTTGTGAGGCTGTCTCAAACTCTGACCTCAGGT 1140
 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATACAGGCGTGAGCCACCTCACCAG 1200
 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATACAGGCGTGAGCCACCTCACCAG 1200
 1201 CGGCTAAATTAGATAAAAAATATAGCAATGGGGGTCTTGCTATGTGCCCCAGGCT 1260
 1201 CGGCTAAATTAGATAAAAAATATAGCAATGGGGGTCTTGCTATGTGCCCCAGGCT 1260
 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACACCCGAGTCA 1320
 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACACCCGAGTCA 1320
 1321 CATTTTTTAAACAGTTACATCTTTATTTAGTATACAGAAAGTAAATACATAAATCT 1380
 1321 CATTTTTTAAACAGTTACATCTTTATTTAGTATACAGAAAGTAAATACATAAATCT 1380
 1381 CAACTGCAATTCAGTAGTAACAGAGTTCTTTTATTAATCTTTTAAACAAAGCTTTAGAG 1440
 1381 CAACTGCAATTCAGTAGTAACAGAGTTCTTTTATTAATCTTTTAAACAAAGCTTTAGAG 1440
 1441 CA 1442
 1441 CA 1442

RESULT 4
 AB223236
 ID AB223236 standard; DNA; 1442 BP.
 AC
 XX
 AC
 XX
 AC
 XX
 24-MAR-2003 (first entry)
 DE Nucleotide sequence of human neuronal thread protein AD7c-NTP.
 XX
 KW Human; neuronal thread protein; AD7c-NTP; Alzheimer's disease; histone;
 KW neurodegeneration; in vivo gene expression; amphipathic compound;
 XX gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key
 CDS 15..1142
 FT
 FT /*tag= a
 FT /product= "neuronal thread protein AD7c-NTP"
 XX
 XX WO200299036-A2.
 XX
 PD 12-DEC-2002.
 XX
 XX 28-MAY-2002; 2002WO-US016429.
 XX
 XX 01-JUN-2001; 2001US-00872968.
 XX

(RHOD-) RHODE ISLAND HOSPITAL.
 Wands JR, De La Monte SM;
 WPI; 2003-140605/13.
 P-PSDB; ABB99774.
 Inducing prolonged in vivo gene expression in mammal by contacting neuronal tissue with composition comprising Alzheimer's disease-associated neural thread protein 7c antisense nucleic acid, histone, amphipathic compound.
 Disclosure; Page 34-35; 69pp; English.
 The present sequence encodes a human neuronal thread protein AD7c-NTP. AD7c-NTP is overexpressed in brains with Alzheimer's disease at early and intermediate stages of neurodegeneration. The expression of AD7c-NTP may be reduced using the method of the invention. The specification describes a method for inducing prolonged in vivo gene expression in a mammal. The method comprises contacting a non-muscular tissue with a composition comprising a nucleic acid, histone and an amphipathic compound. The method is useful for inducing prolonged in vivo gene expression in non-muscular tissue of a mammal, e.g. neuronal tissue, central nervous system (CNS) tissue, tissue comprising a post-mitotic neuronal cell, cortical neuronal cell or hippocampal neuronal cell, glial cell, or vascular endothelial cell. The method is useful in gene therapy applications to treat Alzheimer's disease, where the composition comprises antisense AD7c-NTP nucleic acid
 Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1442; DB 8; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTTGTGAGATGGAGTTTTCGCTCTTGTGCGCCAGGCTGAGTCAATGGCGCAA 60
 DB 1 TTTTGTGAGATGGAGTTTTCGCTCTTGTGCGCCAGGCTGAGTCAATGGCGCAA 60
 QY 61 TCTAGCTCACCGCAACCTCCGCGCTCCCGGGTTCAGGCGATTCCTGCTCAGCCTCC 120
 DB 61 TCTAGCTCACCGCAACCTCCGCGCTCCCGGGTTCAGGCGATTCCTGCTCAGCCTCC 120
 QY 121 CAGTAGCTGGGATTAACAGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTATAG 180
 DB 121 CAGTAGCTGGGATTAACAGCATGTGCACCCAGCTCGGCTAAATTTTGTATTTTATAG 180
 QY 181 TAGAGATGGAGTTTCTCCATGTTGCTCAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
 DB 181 TAGAGATGGAGTTTCTCCATGTTGCTCAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
 QY 241 CCTCGCTCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCATGCGCGGCTTGGC 300
 DB 241 CCTCGCTCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCATGCGCGGCTTGGC 300
 QY 301 TGGCTAAATTTTGTGTTAGAAACAGGTTTCACTCATGTGCCCAAGCTGCTCTCTGAGC 360
 DB 301 TGGCTAAATTTTGTGTTAGAAACAGGTTTCACTCATGTGCCCAAGCTGCTCTCTGAGC 360
 QY 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
 DB 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
 QY 421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
 DB 421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
 QY 481 TGCAGTGTGTGATCACAGCTCACCTGAGCGCTTCACTCTGAGATCAAGCATCTCTCTG 540
 DB 481 TGCAGTGTGTGATCACAGCTCACCTGAGCGCTTCACTCTGAGATCAAGCATCTCTCTG 540
 QY 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACACCTTACACCTGGCTAAATTTTATA 600

Db 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGCTAATTTT 600
 Qy 601 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
 Db 601 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
 Qy 661 GCGCAATCTTGGCTCAGTCACTGCAACCTCTGCTCCGGGTTCAAGTTATTTCTCTGCCCA 720
 Db 661 GCGCAATCTTGGCTCAGTCACTGCAACCTCTGCTCCGGGTTCAAGTTATTTCTCTGCCCA 720
 Qy 721 GCTCTCTAGTAGCTGGGACTACAGCGCCCAACAGCTAGCTAGCTAGCTAGCTAGCT 780
 Db 721 GCTCTCTAGTAGCTGGGACTACAGCGCCCAACAGCTAGCTAGCTAGCTAGCTAGCT 780
 Qy 781 TAGTAGAGATGGGTTTCAACATGTTGCCAGGTTGATCTTGATCTCTGGACCTTGTGATC 840
 Db 781 TAGTAGAGATGGGTTTCAACATGTTGCCAGGTTGATCTTGATCTCTGGACCTTGTGATC 840
 Qy 841 TGCTGCTCTGCGCTCCCAAGTGTCTGGATTTACAGGGGTGAGCCACACGCGCGCTTA 900
 Db 841 TGCTGCTCTGCGCTCCCAAGTGTCTGGATTTACAGGGGTGAGCCACACGCGCGCTTA 900
 Qy 901 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 960
 Db 901 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 960
 Qy 961 GSCCAATCTGCGCTCAGTCACTGCAACCTCTGCTCCGGGCTCAAGGATTTCTCTGCTCA 1020
 Db 961 GSCCAATCTGCGCTCAGTCACTGCAACCTCTGCTCCGGGCTCAAGGATTTCTCTGCTCA 1020
 Qy 1021 GCTCTCAGAGCTGGGATTTAGGGCACTCTGCAACCTCTGCTCCGGGCTCAAGGATTT 1080
 Db 1021 GCTCTCAGAGCTGGGATTTAGGGCACTCTGCAACCTCTGCTCCGGGCTCAAGGATTT 1080
 Qy 1081 TCATTAGAGCGGGGTTTCAACATATTTGTCAGGCTGGTCTCAAACTCTGACCTCAGT 1140
 Db 1081 TCATTAGAGCGGGGTTTCAACATATTTGTCAGGCTGGTCTCAAACTCTGACCTCAGT 1140
 Qy 1141 GACCACTGCTCAGCTTCAAGTGTCTGGATTTACAGGGGTGAGCCACCTCAACCG 1200
 Db 1141 GACCACTGCTCAGCTTCAAGTGTCTGGATTTACAGGGGTGAGCCACCTCAACCG 1200
 Qy 1201 CCGGCTAAATTTAGATAAATAATATGTAGCAATGCTGGGCTCTTGTATGTTGCCAGGCT 1260
 Db 1201 CCGGCTAAATTTAGATAAATAATATGTAGCAATGCTGGGCTCTTGTATGTTGCCAGGCT 1260
 Qy 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCTCA 1320
 Db 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCTCA 1320
 Qy 1321 CATTTTAAACAGTTACATCTTTATTTTAGTATATCTAGAAATGATTAATAAATGAT 1380
 Db 1321 CATTTTAAACAGTTACATCTTTATTTTAGTATATCTAGAAATGATTAATAAATGAT 1380
 Qy 1381 CAAACTGCAATTCAGTAGTAACAGAGTCTTTTATATCTTTTAAACAAAGCTTTAGAG 1440
 Db 1381 CAAACTGCAATTCAGTAGTAACAGAGTCTTTTATATCTTTTAAACAAAGCTTTAGAG 1440
 Qy 1441 CA 1442
 Db 1441 CA 1442

RESULT 5
 AAL54224
 ID AAL54224 standard; DNA; 1442 BP.
 XX
 AC AAL54224;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE AD7C-neural thread protein encoding DNA.
 XX

KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease;
 XX gene; db.
 OS Unidentified.
 XX WO200292115-A2.
 XX 21-NOV-2002.
 XX 16-MAY-2002; 2002WO-CA000712.
 XX 16-MAY-2001; 2001US-0290971P.
 XX (NYMO-) NYMOX CORP.
 XX Averbach PA;
 XX WPI: 2003-129234/12.
 XX P-PSDB; AB19445.
 PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX Disclosure; Fig 1; 60pp; English.
 XX The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This polynucleotide sequence
 CC represents the DNA encoding the AD7C-NTP protein relating to the
 CC invention
 XX
 SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1442; DB 8; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 60
 Db 1 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 60
 Qy 61 TCTCAGCTCAGCGCAACCTCCGCTCTCCGGGTTCAAGGATTTCTCTGCTCAGCTCCC 120
 Db 61 TCTCAGCTCAGCGCAACCTCCGCTCTCCGGGTTCAAGGATTTCTCTGCTCAGCTCCC 120
 Qy 121 CAGTAGCTGGGATTTACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTATTTT 180
 Db 121 CAGTAGCTGGGATTTACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTATTTT 180
 Qy 181 TAGAGATGGATTTCTCCATGTTGCTCAGGCTGGTCTCGAACTCCCGACCTCAGATGTC 240
 Db 181 TAGAGATGGATTTCTCCATGTTGCTCAGGCTGGTCTCGAACTCCCGACCTCAGATGTC 240
 Qy 241 CCTCGTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
 Db 241 CCTCGTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
 Qy 301 TGGCTAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGCTCTCTGAGC 360
 Db 301 TGGCTAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGCTCTCTGAGC 360
 Qy 361 TCAAGCAGTCCACCTGCTCCCAAGTGTGCGATTTACAGGCGTGCAGCGCTGC 420
 Db 361 TCAAGCAGTCCACCTGCTCCCAAGTGTGCGATTTACAGGCGTGCAGCGCTGC 420
 Qy 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 480
 Db 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 480

SQ	Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1442; DB 10; Length 1442;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTTTCTTTTTCAGATGGAGTTTCGCTCTGTCGCCAGGCTGGAGTGCATGGCGAA 60	
DB	1 TTTTCTTTTTCAGATGGAGTTTCGCTCTGTCGCCAGGCTGGAGTGCATGGCGAA 60	
QY	61 TCTCAGCTCACGCCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGGCTCCC 120	
DB	61 TCTCAGCTCACGCCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGGCTCCC 120	
QY	121 CAGTAGCTGGGATTCAGGCGATGTGCAACCGCTCGGGTTCAAGCGATTCTCTGCTCAGGCTCCC 180	
DB	121 CAGTAGCTGGGATTCAGGCGATGTGCAACCGCTCGGGTTCAAGCGATTCTCTGCTCAGGCTCCC 180	
QY	181 TAGAGATGGAGTTTCTCCATGTTGGTTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240	
DB	181 TAGAGATGGAGTTTCTCCATGTTGGTTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240	
QY	241 CCTCGCTCTCGGCTCCCAAGTGTCTAGATACAGGACTGGCCACCATGCGGCTCTGCC 300	
DB	241 CCTCGCTCTCGGCTCCCAAGTGTCTAGATACAGGACTGGCCACCATGCGGCTCTGCC 300	
QY	301 TGGCTAATTTTGTGTGTAAGAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTCTGAGC 360	
DB	301 TGGCTAATTTTGTGTGTAAGAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTCTGAGC 360	
QY	361 TCAAGCAGTCCACCTCGCTCAGCTCCCAAGTGTCTGGATTTACAGGCGTGCAGCGTGC 420	
DB	361 TCAAGCAGTCCACCTCGCTCAGCTCCCAAGTGTCTGGATTTACAGGCGTGCAGCGTGC 420	
QY	421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480	
DB	421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480	
QY	481 TGCAGTGTGTGATTCACAGCTCAGTGCAGGCTTCAACTCTCTGAGATCAAGATCTCTCCTG 540	
DB	481 TGCAGTGTGTGATTCACAGCTCAGTGCAGGCTTCAACTCTCTGAGATCAAGATCTCTCCTG 540	
QY	541 CTTACGCTCCCAAGTGTGGACCAAGAGATGCACCACTACACCTGGCTTAATTTTAA 600	
DB	541 CTTACGCTCCCAAGTGTGGACCAAGAGATGCACCACTACACCTGGCTTAATTTTAA 600	
QY	601 TTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAGTGCAGT 660	
DB	601 TTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAGTGCAGT 660	
QY	661 GGGCGAATCTTGGCTCAGTGCAGCTCTGCTCCCGGGTTCAAGTATTTCTCTGCGCCA 720	
DB	661 GGGCGAATCTTGGCTCAGTGCAGCTCTGCTCCCGGGTTCAAGTATTTCTCTGCGCCA 720	
QY	721 GCTCTCTGAGTGTGGAGTACAGCGCCCAACAGCTAGCTAATTTTGTATTTT 780	
DB	721 GCTCTCTGAGTGTGGAGTACAGCGCCCAACAGCTAGCTAATTTTGTATTTT 780	
QY	781 TAGTAGAGATGGGGTTTCAACATGTTCCGCAAGTGTGATCTTGGACCTTGTGATC 840	
DB	781 TAGTAGAGATGGGGTTTCAACATGTTCCGCAAGTGTGATCTTGGACCTTGTGATC 840	
QY	841 TGGCTGCTCGGCTCCCAAGTGTCTGGATTTACAGGCGTGCAGCCAGCGCGGCTTAA 900	
DB	841 TGGCTGCTCGGCTCCCAAGTGTCTGGATTTACAGGCGTGCAGCCAGCGCGGCTTAA 900	
QY	901 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATACCCAGGCTGGAGTGCAT 960	
DB	901 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATACCCAGGCTGGAGTGCAT 960	
QY	961 GGCCAAATCTCGGCTCACTGCACCTCTGCTCCCGGGCTCAAGCGATTTCTCTGTCTCA 1020	
DB	961 GGCCAAATCTCGGCTCACTGCACCTCTGCTCCCGGGCTCAAGCGATTTCTCTGTCTCA 1020	

QY	1021 GCCTCCCAAGCAGCTGGGATTAACGGGACACCTGCCACACACCCCGCTAATTTTGTATTT 1080	
DB	1021 GCCTCCCAAGCAGCTGGGATTAACGGGACACCTGCCACACACCCCGCTAATTTTGTATTT 1080	
QY	1081 TCATTTAGAGGGGGGTTTTCACCATATTTTGTTCAGGCTGGTCTCAAACTCCTGACCTCAGGT 1140	
DB	1081 TCATTTAGAGGGGGGTTTTCACCATATTTTGTTCAGGCTGGTCTCAAACTCCTGACCTCAGGT 1140	
QY	1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTTACAGGCGTGCAGCACTCAACCCAG 1200	
DB	1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTTACAGGCGTGCAGCACTCAACCCAG 1200	
QY	1201 CGGGCTAATTTAGATATAAAATATGTAGCAATGGGGGCTCTTGTATGTTGCCAGGCT 1260	
DB	1201 CGGGCTAATTTAGATATAAAATATGTAGCAATGGGGGCTCTTGTATGTTGCCAGGCT 1260	
QY	1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACAAACCCAGCCAGTCA 1320	
DB	1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACAAACCCAGCCAGTCA 1320	
QY	1321 CATTTTAAACAGTTACATCTTTTATTTTAGTATATCTAGAAAGTAAATACATATGAT 1380	
DB	1321 CATTTTAAACAGTTACATCTTTTATTTTAGTATATCTAGAAAGTAAATACATATGAT 1380	
QY	1381 CAACCTGCAAAATTCAGTAGTAACAGAGTCTTTTATAAATTTTAAACAAAGCTTTAGAG 1440	
DB	1381 CAACCTGCAAAATTCAGTAGTAACAGAGTCTTTTATAAATTTTAAACAAAGCTTTAGAG 1440	
QY	1441 CA 1442	
DB	1441 CA 1442	

RESULT 7	
ACC84453	
ID	ACC84453 standard; DNA; 1442 BP.
XX	ACC84453;
XX	28-AUG-2003 (first entry)
XX	AD7c-NTP encoding sequence.
DE	Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW	neural thread protein; NTP; tumour; ds.
XX	Unidentified.
XX	WO2003008443-A2.
XX	30-JAN-2003.
XX	19-JUL-2002; 2002WO-CA001105.
XX	19-JUL-2001; 2001US-0306150P.
XX	19-JUL-2001; 2001US-0306161P.
XX	16-NOV-2001; 2001US-0331477P.
XX	(NYMO-) NYMOX CORP.
XX	Averback PA;
XX	WPI; 2003-247999/24.
XX	Novel neural thread protein peptide, referred as cell death peptide,
XX	useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
XX	atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX	Disclosure; Fig 1; 77pp; English.
XX	The present invention relates to a neural thread protein (NTP) peptide
CC	referred to as cell death peptide. Thought to be cytostatic,

antibacterial, immunosuppressive and antiinflammatory. It is useful for treating a condition in a patient requiring removal or destruction of cells, for treating a condition such as benign or malignant tumor, inflammatory disease, autoimmune disease and infectious disease. The peptide useful for treatment is derived from the amino acid sequence of a pancreatic thread protein. The peptide is conjugated, linked or bound to a molecule chosen from antibody or its fragment, antibody-like binding molecule, where the molecule has a higher affinity for binding to a tumor or other target than binding to other cells. Treatment using NTP peptides can remove benign tumors with less risk and fewer of the undesirable side effects of surgery. The present sequence is an NTP encoding sequence

Query Match		100.0%;	Score 1442;	DB 10;	Length 1442;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1442;		Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
Qy	1	TTTTTTTTTTTGAGATGAGATTTTCGCTCTTGTGTCCTCAGGCTGAGTGCATGCGGCAA	60		
Db	1	TTTTTTTTTTTGAGATGAGATTTTCGCTCTTGTGTCCTCAGGCTGAGTGCATGCGGCAA	60		
Qy	61	TCTCAGCTCACGCAACCTCCGCTCCCGGTTCAAGCGATTCCTCGCTCAGGCTCC	120		
Db	61	TCTCAGCTCACGCAACCTCCGCTCCCGGTTCAAGCGATTCCTCGCTCAGGCTCC	120		
Qy	121	CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTGTATTTTTTTTAG	180		
Db	121	CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAAATTTGTATTTTTTTTAG	180		
Qy	181	TAGAGATGGAGTTTCTCATGTTGGTCAAGCTGTCTCGAATCCCGAAGCTCAGATGATC	240		
Db	181	TAGAGATGGAGTTTCTCATGTTGGTCAAGCTGTCTCGAATCCCGAAGCTCAGATGATC	240		
Qy	241	CTCCGCTCGGCTCCCAAAGTGTAGATACAGACTGGGCCACATGCCGGCTCTGCC	300		
Db	241	CTCCGCTCGGCTCCCAAAGTGTAGATACAGACTGGGCCACATGCCGGCTCTGCC	300		
Qy	301	TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGTCTCTGAGC	360		
Db	301	TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGTCTCTGAGC	360		
Qy	361	TCAAGCAGTCCAACCTGAGCTCAGCTCCCAAAGTGTGGGATTCAGGCGTGAGCGGTGC	420		
Db	361	TCAAGCAGTCCAACCTGAGCTCAGCTCCCAAAGTGTGGGATTCAGGCGTGAGCGGTGC	420		
Qy	421	CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	480		
Db	421	CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	480		
Qy	481	TGCAGTGGTGTGATCACAGCTCACTCGAGCCTTCAACTCTCTGAGATCAAGCATCTCTCG	540		
Db	481	TGCAGTGGTGTGATCACAGCTCACTCGAGCCTTCAACTCTCTGAGATCAAGCATCTCTCG	540		
Qy	541	CCTCAGCCTCCCAAGTAGTGGGACCAAGAATGCACCACTACACCTGGCTAAATTTT	600		
Db	541	CCTCAGCCTCCCAAGTAGTGGGACCAAGAATGCACCACTACACCTGGCTAAATTTT	600		
Qy	601	TTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	660		
Db	601	TTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	660		
Qy	661	GGCGAATCTTGGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTCCTCGGCCCA	720		
Db	661	GGCGAATCTTGGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTCCTCGGCCCA	720		
Qy	721	GCCTCTCTGAGTAGCTGGGATTCACAGGGGCCCAACCAAGCTAGCTAAATTTTGTATTTT	780		
Db	721	GCCTCTCTGAGTAGCTGGGATTCACAGGGGCCCAACCAAGCTAGCTAAATTTTGTATTTT	780		
Qy	781	TAGTAGAGATGGGTTTCAAGTTTGGCAGGTTGATCTTGATCTCTGGAATCTGTGATC	840		
Db	781	TAGTAGAGATGGGTTTCAAGTTTGGCAGGTTGATCTTGATCTCTGGAATCTGTGATC	840		

RESULT 8	
ADRI14408	
ID	ADRI14408 standard; DNA; 1442 BP.
XX	
XX	ADR14408;
XX	
XX	21-OCT-2004 (first entry)
XX	
DE	Human NF-kappaB pathway-associated gene SeqID409.
XX	
XX	NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
XX	antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW	antiarteriosclerotic; immunomodulator; cerebroprotective; vasotrophic;
KW	immunosuppressive; vulnery; gene therapy; immune disorder;
KW	inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW	hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW	hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW	X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW	viral infection; HIV-1; hepatitis B; hepatitis C; EBV; influenza;
KW	viral replication; host cell survival; evasion of immune response;
KW	rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW	atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW	autoimmune disorder; hyper immune activity;
KW	aberrant acute phase response; hypercongenital condition; birth defect;
KW	neurotic lesion; wound; organ transplant rejection;
KW	aberrant signal transduction; proliferating disorder; cancer;
KW	HIV propagation; gene; ds: human

XX Homo sapiens.
 XX WO2004065577-A2.
 XX PD 05-AUG-2004.
 XX 13-JAN-2004; 2004WO-US000798.
 XX 14-JAN-2003; 2003US-0440068P.
 XX PR 12-MAY-2003; 2003US-0469757P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 XX WPI; 2004-562168/54.
 XX DR P-PSDB; ADR14409.
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX Claim 1; SEQ ID NO 409; 237pp; English.
 XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an anti-inflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human gene which is
 CC subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;

Query Match 100.0%; Score 1442; DB 13; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

181 TAGAGATGGAGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
 241 CCTCCGTTCTCGGCTTCCCAAAAGTCTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
 241 CCTCCGTTCTCGGCTTCCCAAAAGTCTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
 301 TGGCTAAATTTTGGTGTAGAAACAGGGTTTCACTGATGTGCCAGCTGGTCTCCTGAGC 360
 301 TGGCTAAATTTTGGTGTAGAAACAGGGTTTCACTGATGTGCCAGCTGGTCTCCTGAGC 360
 361 TCAAGCAGTCCACCTGCTCAGCCCTCCCAAAAGTGTGGGATTTACAGGCGTGCAGCCGTGC 420
 361 TCAAGCAGTCCACCTGCTCAGCCCTCCCAAAAGTGTGGGATTTACAGGCGTGCAGCCGTGC 420
 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
 481 TGCAGTGTGTGATCAGAGCTCACTGAGCCTTCAACTCTCTGAGATCAGCATCTCTCTG 540
 481 TGCAGTGTGTGATCAGAGCTCACTGAGCCTTCAACTCTCTGAGATCAGCATCTCTCTG 540
 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACACTACACCTGGCTTAAATTTT 600
 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACACTACACCTGGCTTAAATTTT 600
 601 TTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
 601 TTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
 661 GGCGCAATTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCA 720
 661 GGCGCAATTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCA 720
 721 GCCTCTCAGTAGCTGGGACTACAGGCCCCACACACGCTAGCTAATTTTGTATTTT 780
 721 GCCTCTCAGTAGCTGGGACTACAGGCCCCACACACGCTAGCTAATTTTGTATTTT 780
 781 TAGTAGAGATGGGTTTCAACATGTTTGCAGGTTGATCTTGATCTCTGAGCTTGTGATC 840
 781 TAGTAGAGATGGGTTTCAACATGTTTGCAGGTTGATCTTGATCTCTGAGCTTGTGATC 840
 841 TGCCTGCTCCGCTCCCAAGTGTGGGATTTACAGGCGTGCAGCCACCCCGGGCTTA 900
 841 TGCCTGCTCCGCTCCCAAGTGTGGGATTTACAGGCGTGCAGCCACCCCGGGCTTA 900
 901 TTTTAAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 901 TTTTAAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGGATTTCTCTCTCA 1020
 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGGATTTCTCTCTCA 1020
 1021 GCCTCCCAAGCAGCTGGGATTTACAGGCGCTCCCAACCTCTCTCTCTCTCTCTCTCT 1080
 1021 GCCTCCCAAGCAGCTGGGATTTACAGGCGCTCCCAACCTCTCTCTCTCTCTCTCTCT 1080
 1081 TCATTAGAGCGGGGTTTTCACATATTTGTGAGGCTGGTCTCAAACTCTCTGACCTCAGT 1140
 1081 TCATTAGAGCGGGGTTTTCACATATTTGTGAGGCTGGTCTCAAACTCTCTGACCTCAGT 1140
 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTTACAGGCGTGCAGCCACCTCA 1200
 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTTACAGGCGTGCAGCCACCTCA 1200
 1201 CGGCTAAATTTAGATATAAAATATATGTAGCAATGGGGGCTCTGCTATGTGCCCCAGGCT 1260
 1201 CGGCTAAATTTAGATATAAAATATATGTAGCAATGGGGGCTCTGCTATGTGCCCCAGGCT 1260
 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGGCCACCAACACCCAGCAGTCA 1320
 1261 GGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGGCCACCAACACCCAGCAGTCA 1320

QY 1321 CAATTTTAAACAGTACATCTTTATTTTAGTATATACTAGAAAGTAATAACAATAAATGT 1380
 Db 1321 CAATTTTAAACAGTACATCTTTATTTTAGTATATACTAGAAAGTAATAACAATAAATGT 1380
 QY 1381 CAAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATAAATCTTTTAAACAAAGCTTTAGAG 1440
 Db 1381 CAAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATAAATCTTTTAAACAAAGCTTTAGAG 1440
 QY 1441 CA 1442
 Db 1441 CA 1442

RESULT 9
 AAT27738
 ID AAT27738 standard; DNA; 1418 BP.
 XX AAT27738;
 AC 13-NOV-1996 (first entry)
 DT Neural thread protein coding sequence.
 XX
 DE Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
 KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
 KW binding fragment; ds.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 CDS 14..1207
 FT /*tag= a
 FT /product= "Neural thread protein."
 XX
 XX WO9615272-A1.
 PN 23-MAY-1996.
 PD 14-NOV-1995; 95WO-US017111.
 XX 14-NOV-1994; 94US-00340426.
 PR (GEO) GEN HOSPITAL CORP.
 XX De La Monte S, Wands JR;
 XX WPI; 1996-259865/26.
 DR P-PSDB; AAR95913.

PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
 also NTP DNA and protein sequences used in gene and anti:sense therapy.
 XX
 PS Claim 24; Page 168-170; 238pp; English.

XX A method for detecting the presence of neural thread protein (NTP) having
 CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
 CC comprises (a) contacting a sample from a human subject that is suspected
 CC of containing the NTP with at least one molecule capable of binding to
 CC the protein; and (b) detecting any of the molecule bound to the protein.
 CC The binding molecule is selected from an antibody free of natural
 CC impurities, a monoclonal antibody or a binding fragment of either of
 CC these. The method may be used for diagnosing the presence of Alzheimer's
 CC disease, neuroectodermal tumours and a malignant astrocytoma in a human
 CC
 SQ Sequence 1418 BP; 302 A; 396 C; 315 G; 405 T; 0 U; 0 Other;

Query Match 84.8%; Score 1223.4; DB 2; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 31; Mismatches 13; Gaps 12;
 QY 2 TTTTATTTTGAAGTGGAGTTTCGCTCTTGTGGCCAGGCTGGAGTGAATGGCGCAAT 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 TTTTATTTTGAAGTGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGAATGGCGCAAT 60
 QY 62 CTCAGCTCACCCGCAACCTCCCGGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCCTCCCC 121
 Db 61 CTCAGCTCACCCGCAACCTCCCGGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCCTCCCC 120
 QY 122 AGTA-CTGTGGGATTACAGGCATGTGCAACCCAGCTCGGCTAAATTTTGTATTTTTTTTAG 180
 Db 121 AGTAGGCTGGATTACAGGCATGTGCA-CCACGCTCGGCTAAATTTTGTATTTTTTTTAG 179
 QY 181 TAGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTCGAACTCCCGAATCTCAGATGATC 240
 Db 180 TAGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTCGAACT-CCGACCTCAGATGATC 238
 QY 241 CCTCCGCTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCAATGCCCG-CTCTGC 299
 Db 239 CTCCCGCTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCAATGCCCGCTCTGC 298
 QY 300 CTGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTCGAG 359
 Db 299 CTGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTCGAG 358
 QY 360 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGGGTGAGCGGTG 419
 Db 359 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGGGTGAGCGGTG 418
 QY 420 CCGTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 479
 Db 419 CCGTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 478
 QY 480 GTGAGTGGTGTGATCAGAGCTCACTGAGCGCTTCAACTCTCTGAGATCAAGCATCTCTCT 539
 Db 479 GTGAGTGGTGTGATCAGAGCTCACTGAGCGCTTCAACT-CTGAGATCAAGCATCTCTCT 537
 QY 540 GCCTCAGCTCCC-AAGTAGTGGGACCAAGATGACACCTACCTACCTGCGTAATTTT 598
 Db 538 GCCTCAGCTCCCAGTGGGACCAAGATGACACCTACCTACCTGCGTAATTTT 597
 QY 599 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 658
 Db 598 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 657
 QY 659 GTGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCGCC 718
 Db 658 GTGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCGCC 717
 QY 719 CAGCTCTCTGAGTAGTGGGACTACAGCGCCCAACAGCTAGCTAAATTTTGTGATTT 778
 Db 718 CAGCTCTCTGAGTAGTGGGACTACAGCGCCCAACAGCTAGCTAAATTTTGTGATTT 777
 QY 779 TTTAGTAGAGATGGGG-TTCACCATGTTGCCAGGTTGAT-CTTGATCTCTGAGCTTGT 836
 Db 778 TTTAGTAGAGATGGGGTTTACCATTGTCAGGTTGATGCTAGATCTCTTGACCTTGT 837
 QY 837 GATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGG-CGTGAGCCACACAGCGCCG 895
 Db 838 GATCTGCTGCTCGGCTCCCAAGTGTGGGATTACAGGAGGTGAGCGCCACCGCCG 897
 QY 896 GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 955
 Db 898 GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 957
 QY 956 GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAGCGATTCTCTCG 1015
 Db 958 GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAGCGATTCTCTCG 1017
 QY 1016 TCTCAGCTCCCAAGCAGCTGGGATTACGGGCACTGCGCACCAACCGCTAAATTTTGT 1075
 Db 1018 TCTCAGCTCCCAAGCAGCTGGGATTACGGGCACTG-CACACACCGCTAAATTTTGT 1076
 QY 1076 TATTTTATTTAGCGGGTTTACCATATTTTGTGAGGCTGGTCTCAAACTCTGAGCT 1135
 Db 1077 TATTTTATTTAGCGGGTTTACCATATTTTGTGAGGCTGGTCTCAAACTCTGAGCT 1136

QY 1136 CAGGTGACCCAGCTGCTCAGCTTCCAAAGTGTGGGATTACAGCGTGAGCCACCTCA 1195
 Db |||||
 QY 1137 CAGGTGACCCAGCTGCTCAGCTTCCAAAGTGTGGGATTACAGCGTGGA--CGCCTCA 1194
 Db |||||
 QY 1196 CCAGCGCGCTAATTATAGATAAAAAAATATGTAGCAATGGGGGTCTTGTCTATGTGCC 1255
 Db |||||
 QY 1195 CCAGCGCGCTAATTATAGATAAAAAAATATGTAGCAATGGGGGTCTTGTCTATGTGCC 1254
 Db |||||
 QY 1256 AGGCTGGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACAACCCAGCC 1315
 Db |||||
 QY 1255 AGGCTGGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACAACCCAGCC 1314
 Db |||||
 QY 1316 AGTCACATTTTAAACAGTTACATCTTTATTTAGTATACAGCAATGAGTAATACATAAA 1375
 Db |||||
 QY 1315 AGTCACA-TTTTAAACAGTTACATCTTTATTTAGTATACAGCAATGAGTAATACATAAC 1373
 Db |||||
 QY 1376 CATGTCAAACCTGCAAAATTCAGTAGTAACAGAGTCTTTT 1414
 Db |||||
 QY 1374 ATGGCGGAACCTGCAAAATTCGAGTAGTACAGAGTCTTTT 1412
 Db |||||

RESULT 10

AAQ77883
 ID AAQ77883 standard; cDNA; 1381 BP.

AC AAQ77883;
 XX
 XX 25-MAR-2003 (revised)
 DT 06-JUL-1995 (first entry)
 XX
 XX Neural thread protein AD10-7 cDNA.
 XX
 XX Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
 KW malignant astrocytomas; glioblastomas; ss.
 XX
 XX Rattus rattus.
 OS
 XX
 XX WO9423756-A1.
 XX
 XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US004321.
 XX
 XX 20-APR-1993; 93US-00050559.
 PR
 XX (GEO) GEN HOSPITAL CORP.
 PA
 XX De La Monte SM, Wanda JR;
 XX
 XX WPI; 1994-341497/42.
 DR
 XX
 XX Detection of neural thread proteins - to detect sporadic and familial
 PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
 PT glioblastomas (Eng).
 PT
 XX
 XX Example 4; Fig 16R; 158pp; English.
 PS
 XX

CC AAQ77883 is the AD10-7 neural thread protein (NTP) cDNA. This sequence
 CC was used in the development of an antibody dependent method, for the
 CC detection of NTPs. This new method could be used to diagnose Alzheimer's
 CC disease (differentiating between sporadic and familial) neuroectodermal
 CC tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 CC
 XX Sequence 1381 BP; 296 A; 385 C; 301 G; 399 T; 0 U; 0 Other;

Query Match 74.8%; Score 1078.6; DB 2; Length 1381;
 Best Local Similarity 94.3%; Pred. No. 6.3e-279;
 Matches 1316; Conservative 0; Mismatches 54; Indels 25; Gaps 18;
 QY 2 TTTTATTTTGGAGTGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGAATGGCGCAAT 61
 |||||

Db |||||
 QY 1 TTTTATTTTGGAGTGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGAATGGCGCAAT 60
 |||||
 QY 62 CTGAGCTCACCGCAACCTCCCGGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 121
 |||||
 Db 61 CTGAGCTCACCGCAACCTCCCGGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 120
 |||||
 QY 122 AGTAGCTGGGATTACAGGCATGTGCACCGCTCGGCTAAATTTTGTATTTTTTTTACT 181
 |||||
 Db 121 AGTAGCTGGGATTACAGGCATGTGCA-CCAGCTCGGCTAAATTTTGTATTTTTTTTACT 179
 |||||
 QY 182 AGAGATGAGATTTT--CTCCATGTTGGTTCAGGCTGTCTCGAACTCCCGACCTCAGATGAT 239
 |||||
 Db 180 AGAGATGAGATTTTAACTCCATGTTGGTTCAGGCTGTCTCGAACTCCCGACCTCAGATGAT 239
 |||||
 QY 240 CCTCCGCTCGGCTCCCAAAGTGTCT--AGATACAGGACTGGGCCACCATGCCCCGG-CT 295
 |||||
 Db 240 CTCCCGTCTCGGCTCGCCCAAAGTGTCTGAGATTACAGGCATGAGCCACCATGCCCCGGCT 299
 |||||
 QY 296 CTGCTGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATG-TGCCCAAGCTGGTCTC 354
 |||||
 Db 300 CTGCTGCTGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTC 359
 |||||
 QY 355 CTGAGCTCAAGCAGTCCACCTGCTCAGCTCCCAAAGTGTGGGATTACAGGCGTGCAG 414
 |||||
 Db 360 CTGAGCTCAAGCAGTCCACCTGCTCAGCTCCCAAAGTGTGGGATTACAGGCGT-CAG 418
 |||||
 QY 415 CCGTGCCTGGGCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGG 474
 |||||
 Db 419 CCGTGCCTGGGCTTTTATTTTATTTTAAAGACACAGGTGTACCACTCTTACCCAGG 478
 |||||
 QY 475 ATGAAGTCAGTGTGTGATCAGAGTCTCACTGCGAGCTTCAACTCTGAGATCAAGCAAT 533
 |||||
 Db 479 ATGAAGTCAGTGTGTGATCAGAGTCTCACTGCGAGCTTCAACTCTGAGATCAAGCAAT 538
 |||||
 QY 534 CCTCTGCTCAGCCTCCCAAAGTGTGGGACCAAGAGACATGCACACTACACCTGGCTA 593
 |||||
 Db 539 CCTCTGCTCAGCCTCCCAAAGTGTGGGACCAAGAGACATGCACACTACACCTGG-TA 597
 |||||
 QY 594 ATTTTATTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCAGGCTGA 653
 |||||
 Db 598 ATTTTATTTTATTTTAAATTTTGTGAGACAGAGTCTC-ACCTGTGTCAACCAGGCTGA 656
 |||||
 QY 654 GTGCAGTGCGCAATCTTGGCTCAGTCAACCTCTGCTCCCGGTTTCAAGTATTTCTCC 713
 |||||
 Db 657 GTGCAGTGCGCAATCTTGGCTCAGTCAACCTCTGCTCCCGGTTTCAAGTATTTCTCC 716
 |||||
 QY 714 TGCCCCAGCCTCTCTGAGTAGTGGGACTACAGGCGGCCCAACACGCTAGCTAATTTTTT 773
 |||||
 Db 717 TGCCCCAGCCTCTCTGAGTAGTGGGACTACAGGCGGCCCAACACGCTAGCTAATTTTTT 776
 |||||
 QY 774 GTATTTTGTAGTAGATGGGG-TTCAACATGTTGCCAGGTTGATCTTGATCTCTGGACC 832
 |||||
 Db 777 GTATTTTGTAGTAGATGGGGTTTCAACATGTTGCCAGGTTGATCTTGATCTCTTGACC 836
 |||||
 QY 833 TTGTGATCTGCTGCTCGGCT-CCCAAAGTGTGGGATTACAGGCGTGAGGCCACCACG 891
 |||||
 Db 837 TTGTGATCTGCTGCTCGGCTACCCAAAGTGTGGGATTACAG-GTGTGATCTCCAC 894
 |||||
 QY 892 CCGCGCTATTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTATCCAGGCTG 951
 |||||
 Db 895 GCGCGCTATTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTATCCAGGCTG 954
 |||||
 QY 952 GAGTGCAATGGCCAAATCTCGGCTCAGTGCACCTCTGCTCCCGGCTCAGGCAATCT 1011
 |||||
 Db 955 GAGTGCAATGG-CAAAATCTCGGCTACTCGCAACCTCTGCTCCCGG-TCAAGCGATCT 1012
 |||||
 QY 1012 CCGTCTCAGCTCCCAAAGCAGTGGGATTACGGGCACCTGCCACACACCCCGCTAAT 1071
 |||||
 Db 1013 CCGTCTCAGCTCCCAAAGCAGTGGGATTACGGG--ACCTGCACACACACCCCGCTAAT 1070
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 QY 1072 TTTGTATTTTCAATTAGAGCGGGTTTCAACATATTTGTGAGGCT-GGTCTCAAACTCT 1130
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 Db 1071 TTTGTATTTTCAATTAGAGCGGG--TTTACCATAATTTGTGAGGCTGGGTCTCAAACTCT 1128
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Db 31649 TTTGAACTCTTAATCTTCAAGTGTATCCACCCGCTCTGCTCCCAAGTCTGGGATTAC 31590
 QY 1179 AGCGTGAAGCCACCTCACCCAGCC----GGCTAATTTAGATAAAAAAATATGTAGCAATG 1234
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 QY 1235 GGGGCTCTGTATGTGTCGCCAGGCTGTCTCAAACTTCTGCTTCAATGCAATCTTCCA 1294
 Db 31529 CAGGATCTCACTATGTGTCAGACTGGTCTTGAACCTCTGGGCTTAAGGGATCGTCTCTG 31470
 QY 1295 AATGAGCCAC 1304
 Db 31469 TCTCAGCCTC 31460

RESULT 13
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 ID ABL62910 standard; DNA; 65608 BP.
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 AC ABL62910;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Breast cancer related gene sequence SEQ ID NO:1247.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; da.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US010838.
 XX

05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233131P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
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 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PG, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 PS Claim 1; SEQ ID NO 1247; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX
 SQ Sequence 65608 BP; 15987 A; 16979 C; 16761 G; 15878 T; 0 U; 3 Other;
 Query Match 40.8%; Score 587.8; DB 6; Length 65608;
 Best Local Similarity 70.6%; Pred. No. 1.6e-146;
 Matches 940; Conservative 0; Mismatches 347; Indels 44; Gaps 10;
 QY 4 TTTTGTGAGATGGAGTTTTCGCTCTTGTGCCCAGGCTGAGTGCAATGCGCAATCT 63
 Db TTTTGTGAGATGGAGTTTTCGCTCTTGTGCCCAGGCTGAGTGCAATGCGCAATCT 39935
 QY 64 CAGCTCACCGCAACCTCCGCTCCCGGTTTCAAGCGATTCTCTGCTCAGCCTCCCGAG 123
 Db CAGCTCACCGCAACCTCCGCTCCCGGTTTCAAGCGATTCTCTCCTACCTCAGCCTCCCGAG 39875
 QY 124 TAGCTGGGATTTACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTGTAGTAG 183
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 QY 184 AGATGGAGTTTCTCCATGTTGCTCAGGCTGTCTCGAACTCCCGACCTCAGATGATCCT 243
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 QY 244 CCGTCTCGGCTCCCAAGTCTAGATACAGGACTGGCCACATGCCCGGCTCTGCGCTGG 303
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 QY 304 CTAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAGCTGTGCTCTCTGAGCTCA 363
 Db AGTATGAAGCAGTACCTCCGGAATATGACGGGCTCCCAACCCAGCTCTGAAGAGCTC 39640
 QY 364 AGCAGTCCACCTGCTCAGCCTCCCAAGTGTCTGGGATTA----- 403
 Db TTCACCTGTCTGGCTGGGCCACACCACTCAGCTCCACCTAAATGCGGCTGTGTTCTTT 39580

CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. MI can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of MI, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. MI can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX
 SQ Sequence 65608 BP; 15987 A; 16979 C; 16761 G; 15878 T; 0 U; 3 Other;
 Query Match 40.8%; Score 587.8; DB 6; Length 65608;
 Best Local Similarity 70.6%; Pred. No. 1.6e-146;
 Matches 940; Conservative 0; Mismatches 347; Indels 44; Gaps 10;
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 39993 TTTTGTGAGATGAGATTTT-GCTCTTGTGCTCCAGGCTGAGTGCATGCGCAATCT 39935
 64 CAGCTCACCGCAACTCCGCTCCCGGTTCAAGCGATTCCTCGCTCAGCTCCCGAG 123
 39934 CAGCTCACCGCAACTCCGCTCCCGGTTCAAGCGATTCCTCGCTCAGCTCCCGAG 39875
 124 TAGCTGGGATACAGCATGTGACCCAGCTCGCTAAATTTTGTATTTTGTAGTAG 183
 39874 TAGCTGGGATACAGCATGTGACCCAGCTCGCTAAATTTTGTATTTTGTATTTT 39819
 184 AGATGAGATTTCTCCATGTGCTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATCCCT 243
 39818 AGAGGGGTTTCTCCATGTGCTCAGGTTGGTCTTGAACCCCGACCTCAGATGATCCCG 39759
 244 CCGTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCATGCCGGCTCTCGCTGG 303
 39758 CCACCTTGGCTCCCAAGTGTG-GGGATTACAGGTGTGAGTTTACAGAAACATTTA 39700
 304 CTAAATTTTGTGTAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCCTGAGCTCA 363
 39699 AGTATGAAGCATGTAACCTCGGAATATGACGGCTCCCAACCCAGGCTCTGGAAGCTC 39640
 364 AGCAGTCCACCTCGCTCCAGCTCCCAAGTGTGGGATTA----- 403
 39639 TTCACTTGTCTGGCTGGGCGCACCACTCAGCTCCACCTAAACTGGGCTGTCTCTT 39580
 404 CAGGGGTGAGCGGTGCTGGCTTTTATTTTATTTATTTTAAAGACAGAGTGTCCCAAC 463
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 Db 39227 TGGCTAAATTTTGTATTTGTAGTAGAGATGGGTTTCACTATGTAGTCAAGCTGTCTCA 39168
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 Db 39167 AACTCTGACCTCAGAGATCTCTGCTCGGCTCCCAAGTGTGGGATTTACAGCTG 39108
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 Db 38987 GTTCAAGCATTTCTGCTCAGCTCTCCCAAGTAGCTAGGACTACAGGCTGTGCCACC 38928
 Qy 1058 ACACCCGCTAAATTTTGTATTTTATTTAGAGCGGGTTCACATATTTGTGAGGCTG 1117
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 Qy 1118 GTCTCAACTCTGACCTCAGTGCACCTGCTCAGCTCGGCTCCCAAGTGTGGGATTA 1177
 Db 38867 GTCTTGAACCTCTAACTTCAAGTGCATCCCGCTCTGCTCCCAAGTGTGGGATTA 38808
 Qy 1178 CAGGCTGAGCACCTCACCACCGC-----GGCTAATTTAGATAAAAAAATATGTAGCAAT 1233
 Db 38807 CAGGATGAGCACCAACACCTGCGCTCTGCCCACTAATTAATAAAAAAATTTTGTAGAG 38748
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 AC ABL67668;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:6005.
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US010838.
 XX
 PR 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-023133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
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 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
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 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
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 PR 01-NOV-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX PA (AVAL-) AVALON PHARM.
 XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX DR WPI; 2002-188264/24.
 XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX PS Claim 1; SEQ ID NO 6005; 44pp; English.
 XX CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
 CC tumour
 XX SQ Sequence 65608 BP; 15987 A; 16979 C; 16761 G; 15878 T; 0 U; 3 Other;
 Query Match 40.8%; Score 587.8; DB 6; Length 65608;
 Best Local Similarity 70.6%; Pred. No. 1.6e-146;
 Matches 940; Conservative 0; Mismatches 347; Indels 44; Gaps 10;

QY 4 TTTTGTGAGATGAGTGTGCTCTGCTCTGCTCCAGGCTGAGTGCATGCGCAATCT 63
 DB TTTTGTGAGATGAGTGTGCTCTGCTCTGCTCCAGGCTGAGTGCATGCGCAATCT 39935
 QY 64 GAGCTCACCGCAACCTCCGCTCCGCGGTTCAGGGAATCTCTGCTGCTGAGCTCCCGAG 123
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 QY 124 TAGCTGGGATTAAGGCAATGTCACCCAGCTCGGCTAATTTGTTATTTTATTTAGTAG 183
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 DB AGCAGTCCACCTGCTCAGCTCCCAAGTGTGCGGATTA----- 39639
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 DB CAGGCTGAGCGCTGCTGCTGCTTTTATTTTATTTTATTTTAAAGACACAGTGTCCAC 39520
 QY 464 TCTTACCAGGATGAAGTGCAGTGTGATCAGAGCTCAGTGCAGCTTCACTGCTCA 523
 DB TCTTACCAGGATGAAGTGCAGTGTGATCAGAGCTCAGTGCAGCTTCACTGCTCA 39519
 QY 524 GATC-AAGCATCTCTGCTCAGCTCCAGTGTGCGGACTACAGGCGCCACACGCTAG 582
 DB GATC-AAGCATCTCTGCTCAGCTCCAGTGTGCGGACTACAGGCGCCACACGCTAG 39459
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 DB TGAGCCACACGCGCGCTT--ATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTT 39107
 QY 938 TGTTACCAGGCTGAGTGCAGTGGCGCAATCTGCTCACTGCTCACTGCTCCCGG 997
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 QY 1058 ACACCCCGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1117

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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 16:58:08 ; Search time 1049 Seconds
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 14778644

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Listing first 45 summaries

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SUMMARIES

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3	1442	100.0	1442	10	US-09-964-667-1 Sequence 1, Appli
4	1442	100.0	1442	10	US-09-872-968-1 Sequence 1, Appli
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6	1442	100.0	1442	14	US-10-146-130-1 Sequence 1, Appli
7	1442	100.0	1442	14	US-10-092-934-1 Sequence 1, Appli

8	1442	100.0	1442	14	US-10-153-334-53 Sequence 53, Appli
9	1442	100.0	1442	14	US-10-198-069-48 Sequence 48, Appli
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11	1442	100.0	1442	19	US-10-755-889-409 Sequence 409, App
12	1442	100.0	1442	21	US-10-910-173-1 Sequence 1, Appli
13	1223.4	84.8	1418	9	US-09-964-666-4 Sequence 4, Appli
14	1223.4	84.8	1418	9	US-09-964-412-4 Sequence 4, Appli
15	1223.4	84.8	1418	10	US-09-964-667-4 Sequence 4, Appli
16	1223.4	84.8	1418	10	US-09-964-678A-4 Sequence 4, Appli
17	1080.2	74.9	1381	9	US-09-964-666-3 Sequence 3, Appli
18	1080.2	74.9	1381	9	US-09-964-412-3 Sequence 3, Appli
19	1080.2	74.9	1381	10	US-09-964-667-3 Sequence 3, Appli
20	1080.2	74.9	1381	10	US-09-964-678A-3 Sequence 3, Appli
21	590.4	40.9	33112	17	US-10-429-873A-3 Sequence 3, Appli
22	587.8	40.8	65608	9	US-09-962-436-292 Sequence 292, App
23	587.8	40.8	65608	9	US-09-962-832-119 Sequence 119, App
24	587.8	40.8	65608	9	US-09-954-531-180 Sequence 180, App
25	587.8	40.8	65608	21	US-10-843-641A-1247 Sequence 1247, App
26	587.8	40.8	65608	21	US-10-843-641A-2751 Sequence 2751, Ap
27	587.8	40.8	65608	21	US-10-843-641A-6005 Sequence 6005, Ap
28	535.2	37.1	79528	20	US-10-723-860-2621 Sequence 2621, Ap
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32	524.4	36.4	62944	21	US-10-843-641A-5284 Sequence 5284, Ap
33	524.4	36.4	62944	21	US-10-843-641A-6599 Sequence 6599, Ap
34	513.4	35.6	28805	13	US-10-087-192-2008 Sequence 2008, Ap
35	513	35.6	21470	9	US-09-764-847-1157 Sequence 1157, Ap
36	513	35.6	21470	14	US-10-092-154-1157 Sequence 1157, Ap
37	502.8	34.9	75252	13	US-10-087-192-304 Sequence 904, App
38	501	34.7	193691	20	US-10-719-993-6768 Sequence 6768, Ap
39	496.4	34.4	115756	22	US-10-756-149-3838 Sequence 3838, Ap
40	490.8	34.0	166496	22	US-10-756-149-590 Sequence 590, App
41	490.4	34.0	99014	9	US-09-880-107-3428 Sequence 3428, Ap
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ALIGNMENTS

RESULT 1

US-09-964-666-1

; Sequence 1, Application US/09964666

; Patent No. US20020104108A1

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; Wands, Jack R.

; TITLE OF INVENTION: Transgenic Animals and Cell Lines for

; Screening Drugs Effective for the Treatment or Prevention

; of Alzheimer's Disease

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/964,666

; FILING DATE: 28-Sep-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.

; REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1139
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-666-1

Query Match 100.0%; Score 1442; DB 9; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTTCAGATGGAGTTTTCGCTCTTGTGCGCCAGGCTGGAGTGCATATGGCGCA 60
Db 1 TTTTCTTTTTCAGATGGAGTTTTCGCTCTTGTGCGCCAGGCTGGAGTGCATATGGCGCA 60

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Db 661 GCGCAATCTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCA 720

QY 721 GCCTCTGAGTAGTGGGACTACAGGCGCCACGAGCTAGCTAATTTTGTATTTT 780
Db 721 GCCTCTGAGTAGTGGGACTACAGGCGCCACGAGCTAGCTAATTTTGTATTTT 780

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Db 781 TAGTAGAGATGGGTTTCCACATGTTTCGCGAGGTGATCTTGATCTCTGGACCTTGTGATC 840

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Db 1021 GCCTCCCAAGCAGCTGGGATTTACGGGCACTGCGCAACACCCCGCTAATTTTGTATTT 1080

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Db 1081 TCATTAGAGGCGGGTTTTCACATATTTGTGAGGCTGCTCAAACTCTGACCTCAGGT 1140

QY 1141 GACCCACCTGCTCAGGCTTCCAAAGTGTCTGGGATTTACAGGCTGGAGCCACCTCACCCAG 1200
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QY 1201 CCGGCTAAATTTAGATATAAAATATGTAGCAATGGGGGTCTGTCTATGTTGCCAGGCT 1260
Db 1201 CCGGCTAAATTTAGATATAAAATATGTAGCAATGGGGGTCTGTCTATGTTGCCAGGCT 1260

QY 1261 GGTCTCAAACTCTGGCTTCATGCAATCTTCCAAATGAGGCAACACCCAGGCTCA 1320
Db 1261 GGTCTCAAACTCTGGCTTCATGCAATCTTCCAAATGAGGCAACACCCAGGCTCA 1320

QY 1321 CATTTTAAACAGTTACATCTTTATTTAGTACTAGAAAGTAAATAACAATGAATGT 1380
Db 1321 CATTTTAAACAGTTACATCTTTATTTAGTACTAGAAAGTAAATAACAATGAATGT 1380

QY 1381 CAAACCTGCAAAATCAGTAGTAAACAGGCTCTTTTATAAATTTTAAACAGCTTTAGAG 1440
Db 1381 CAAACCTGCAAAATCAGTAGTAAACAGGCTCTTTTATAAATTTTAAACAGCTTTAGAG 1440

QY 1441 CA 1442
Db 1441 CA 1442

RESULT 2
US-09-964-412-1
; Sequence 1, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wanda, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412
 FILING DATE: 28-Sep-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Emond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0609.4370000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1442 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 15..1139
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-964-412-1

Query Match 100.0%; Score 1442; DB 9; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTTTTTTTTTTTCAGATGGAGTTTTCGCTCTGTGTGCCAGGCTGGAGTGCATATGGCGAA	60
DB	1	TTTTTTTTTTTTCAGATGGAGTTTTCGCTCTGTGTGCCAGGCTGGAGTGCATATGGCGAA	60
QY	61	TCTCAGCTCAGCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCC	120
DB	61	TCTCAGCTCAGCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCC	120
QY	121	CAGTAGCTGGGATTCAGGATGTGCAACCGCTCGGCTAAATTTGTTATTTT	180
DB	121	CAGTAGCTGGGATTCAGGATGTGCAACCGCTCGGCTAAATTTGTTATTTT	180
QY	181	TAGAGATGAGTTTCTCCATGTTGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATC	240
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QY	241	CCTCGCTCTCGGCTCCCAAGTGTAGATACAGGACTGGCCACCACTGCGGCTCTGCC	300
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QY	301	TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC	360
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QY	361	TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGATTCAGGCGTGCAGCGGTGC	420
DB	361	TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGATTCAGGCGTGCAGCGGTGC	420
QY	421	CTGGCCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG	480
DB	421	CTGGCCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG	480
QY	481	TGAGTGTGTGATCAGCTCAGTGCAGCTTCACTCTGAGATCAAGCATCTCTCTG	540
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DB	661	GGCGCAATCTCGCTCAGTGCACCTCTCGCTCCCGGGTTCAAGTTATTTCTCTGCCCA	720
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DB	721	GCCTCTCAGTAGCTGGGACTACAGCGCCACACAGCTAGCTAATTTTTTGTATTTT	780
QY	781	TAGTAGAGATGGGGTTCAACATTTGCGCAGGTTGATCTTGATCTCTGGACCTTGTGATC	840
DB	781	TAGTAGAGATGGGGTTCAACATTTGCGCAGGTTGATCTTGATCTCTGGACCTTGTGATC	840
QY	841	TGCTGCTCCTCGGCTCCCAAGTGTGGATTCAGGCGTGCACACCGCCGGCTTA	900
DB	841	TGCTGCTCCTCGGCTCCCAAGTGTGGATTCAGGCGTGCACACCGCCGGCTTA	900
QY	901	TTTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCAT	960
DB	901	TTTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCAT	960
QY	961	GGCCAAATCTCGGCTCAGTGCACCTCTGCTCCCGGCTCAAGCGATTTCTCTGTCTCA	1020
DB	961	GGCCAAATCTCGGCTCAGTGCACCTCTGCTCCCGGCTCAAGCGATTTCTCTGTCTCA	1020
QY	1021	GCCTCCCAAGCAGCTGGGATTCAGGCGCACCTGCGCACACCCCGCTAATTTTGTATTT	1080
DB	1021	GCCTCCCAAGCAGCTGGGATTCAGGCGCACCTGCGCACACCCCGCTAATTTTGTATTT	1080
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DB	1081	TCATTTAGAGCGGGGTTTTCACCATATTTGTTCAGGCTGGTCTCAAACTCTGACCTCAGGT	1140
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DB	1201	CGGCTAATTTAGATAAAAAATATGATAGCAATGGGGGCTTGTCTATGTGCGCCAGGT	1260
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DB	1261	GGTCTCAAACTTCTGGCTTTCATGCAATCTTCCAAATGAGCCACACACCGCCAGTCA	1320
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RESULT 3

US-09-964-667-1

; Sequence 1, Application US/09964667

; Publication No. US2003003621A1

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; Wands, Jack R.

; TITLE OF INVENTION: Transgenic Animals and Cell Lines for

; Screening Drugs Effective for the Treatment or Prevention

; of Alzheimer's Disease

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,667
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Emond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-667-1

Query Match 100.0%; Score 1442; DB 10; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTTTGGAGATGAGTTTTCCTTCTGTTGCTCCAGGCTGAGTGCATATGCGCAA 60
DB 1 TTTTATTTTGGAGATGAGTTTTCCTTCTGTTGCTCCAGGCTGAGTGCATATGCGCAA 60
QY 61 TCTCAGCTCAGCGCAACCTCCGCTCCGCGTTCAAGGATTTCTCCTGCCTCAGCTCCC 120
DB 61 TCTCAGCTCAGCGCAACCTCCGCTCCGCGTTCAAGGATTTCTCCTGCCTCAGCTCCC 120
QY 121 CAGTAGTGGGATTACAGCATATGTCACCCAGCTCGGCTAATTTTGTATTTTGTATTTAG 180
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DB 481 TGCAGTGTGTGATCAGACCTCAGCTGAGCTTTCAACTCCTGAGATCAAGCATCTCCTG 540
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QY 601 TTTTATTTTAAATTTTGGAGACAGAGTCTCAACTCTGTCCACCGAGCTGGAGTGCAGT 660
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DB 1081 TCATTAGAGCGGGGTTTTCACCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGT 1140
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RESULT 4
US-09-872-968-1
; Sequence 1, Application US/09872968
; Publication No. US20030050262A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872,968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2

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SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1442

TYPE: DNA

ORGANISM: Homo sapiens

US-09-872-968-1

Query Match 100.0%; Score 1442; DB 10; Length 1442;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTTTGTGAGATGAGATTTTGGCTCTGTTGTCCTGAGGCTGAGATGCAATGGCGCA 60
 DB 1 TTTTATTTTGTGAGATGAGATTTTGGCTCTGTTGTCCTGAGGCTGAGATGCAATGGCGCA 60
 QY 61 TCTCAGCTCACCAGCACTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 120
 DB 61 TCTCAGCTCACCAGCACTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 120
 QY 121 CAGTAGCTGGGATTCAGGCAATGTGACCCAGCTCGGCTAAATTTTGTATTTTGTATTTAG 180
 DB 121 CAGTAGCTGGGATTCAGGCAATGTGACCCAGCTCGGCTAAATTTTGTATTTTGTATTTAG 180
 QY 181 TAGAGATGAGATTTTCCATTTGTTGTCAGGCTGCTCGAACTCCCGACCTCAGATGATC 240
 DB 181 TAGAGATGAGATTTTCCATTTGTTGTCAGGCTGCTCGAACTCCCGACCTCAGATGATC 240
 QY 241 CCTCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 300
 DB 241 CCTCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 300
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 DB 301 TGGCTAAATTTTGTGTAAGAACAGGTTTCACTGATGTGCCCAAGCTGCTCTCTGAGC 360
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 DB 361 TCAAGCAGTCCACTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 420
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 DB 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
 QY 481 TGCAGTGTGTGATCACAGCTCACTGACGCTTCACTCTGAGATCAAGCATCTCTCTG 540
 DB 481 TGCAGTGTGTGATCACAGCTCACTGACGCTTCACTCTGAGATCAAGCATCTCTCTG 540
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 DB 541 CTTGAGCTTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGCTAAATTTT 600
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 DB 601 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
 QY 661 GCGCAATCTGGCTCACTGCACTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 720
 DB 661 GCGCAATCTGGCTCACTGCACTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 720
 QY 721 GCTCTCTGATGAGTGGGACTACAGGCGCCCAAGCTAGCTAAATTTTGTATTTT 780
 DB 721 GCTCTCTGATGAGTGGGACTACAGGCGCCCAAGCTAGCTAAATTTTGTATTTT 780
 QY 781 TAGTAGATGGGTTTCCATGTTGCGCCAGTGTGATCTTGATCTTGACCTTGTGATC 840
 DB 781 TAGTAGATGGGTTTCCATGTTGCGCCAGTGTGATCTTGATCTTGACCTTGTGATC 840
 QY 841 TGCCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 900
 DB 841 TGCCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 900
 QY 901 TTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 960

DB 901 TTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 QY 961 GCGCAATCTGGCTCACTGCACTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 1020
 DB 961 GCGCAATCTGGCTCACTGCACTCTGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCC 1020
 QY 1021 GCTCTCCCAAGCAGCTGGGATTCAGGCGCACTGCGCCACCAACCCCGCTAAATTTTGTATTT 1080
 DB 1021 GCTCTCCCAAGCAGCTGGGATTCAGGCGCACTGCGCCACCAACCCCGCTAAATTTTGTATTT 1080
 QY 1081 TCATTTAGAGCGGGGTTTCCATATTTGTGAGGCTGCTCAAACTCTGAGCTCAGCTCAGGT 1140
 DB 1081 TCATTTAGAGCGGGGTTTCCATATTTGTGAGGCTGCTCAAACTCTGAGCTCAGCTCAGGT 1140
 QY 1141 GACCCACCTGCTCAGGCTTCCAAAGTGTGCGGATTTACAGGCGTGAGCCACCTCACCCAG 1200
 DB 1141 GACCCACCTGCTCAGGCTTCCAAAGTGTGCGGATTTACAGGCGTGAGCCACCTCACCCAG 1200
 QY 1201 CCGGCTAAATTTAGATAAATAATATGTAGCAATGGGGGTCTTGTCTATGTTGCCAGGCT 1260
 DB 1201 CCGGCTAAATTTAGATAAATAATATGTAGCAATGGGGGTCTTGTCTATGTTGCCAGGCT 1260
 QY 1261 GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACCAACCCAGCCAGTCA 1320
 DB 1261 GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACCAACCCAGCCAGTCA 1320
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 DB 1321 CATTTTAAACAGTTACATCTTTATTTTAGTATATAGAAAGTAAATAAATAAATATGT 1380
 QY 1381 CAAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
 DB 1381 CAAACCTGCAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
 QY 1441 CA 1442
 DB 1441 CA 1442

RESULT 5

US-09-964-678A-1

; Sequence 1, Application US/09964678A

; Publication No. US20030066097A1

; GENERAL INFORMATION:

; APPLICANT: Wands, Jack R.

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs

; TITLE OF INVENTION: Effective for the Treatment or Prevention of

; FILE REFERENCE: 0609.4370002

; CURRENT APPLICATION NUMBER: US/09/964,678A

; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: 09/380,203

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: PCT/US98/03685

; PRIOR FILING DATE: 1998-02-26

; PRIOR APPLICATION NUMBER: 60/038,908

; PRIOR FILING DATE: 1997-02-26

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1442

; TYPE: DNA

; ORGANISM: Unknown

; FEATURES:

; OTHER INFORMATION: AD7c-NTP cDNA

; NAME/KEY: CDS

; LOCATION: (15)..(1139)

; OTHER INFORMATION:

; US-09-964-678A-1

Query Match 100.0%; Score 1442; DB 10; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;

Db 241 |||||CTCGCTCGGCTCCCAAAGTGTAGATACAGGACTGGCCACCAATGCGCGCTCTGCC 300
Qy 301 TGGCTAAATTTTGTGTAGAAACAGGTTTCACTGATGTGCCCAAGCTGTCTCTGAGC 360
Db 301 TGGCTAAATTTTGTGTAGAAACAGGTTTCACTGATGTGCCCAAGCTGTCTCTGAGC 360
Qy 361 TCAAGCAGTCCACCTCGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
Db 361 TCAAGCAGTCCACCTCGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
Qy 421 CTGGCCCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
Db 421 CTGGCCCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
Qy 481 TGCAGTGGTGTATCACAGTCACTGACGCTTCACTCTGATCTCAAGTCAAGCATCTCTCTG 540
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Qy 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGCTAAATTTTA 600
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Db 601 TTTTATTTTAAATTTTGTGAGACAGAGTCTCACTCTGTCAACAGGCTGAGTGCAGT 660
Qy 661 GGGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTATTTCTCTGCCCA 720
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Qy 721 GCCTCTGAGTAGCTGGGACTACAGGCGCCACACCGCTAGCTAATTTTGTATTTT 780
Db 721 GCCTCTGAGTAGCTGGGACTACAGGCGCCACACCGCTAGCTAATTTTGTATTTT 780
Qy 781 TAGTAGAGATGGGTTTCAACATTTGCGCAGGTTGATCTTGATCTCTGCACTTGTGATC 840
Db 781 TAGTAGAGATGGGTTTCAACATTTGCGCAGGTTGATCTTGATCTCTGCACTTGTGATC 840
Qy 841 TGCCTGCTCGGCTCCCAAAGTGTGGGATTTACAGGCGTGAACCAACCGCGGCTTA 900
Db 841 TGCCTGCTCGGCTCCCAAAGTGTGGGATTTACAGGCGTGAACCAACCGCGGCTTA 900
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Db 1021 GCCTCCCAAGCAGTGGGATTTAGGGCACTGCGCTCCCGGGCTCAAGCGATTTTCTATTT 1080
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Db 1141 GACCCACCTGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGAACCACTCTCAACAG 1200
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Db 1201 CCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGTCTTGTATGTTCGCCAGGT 1260
Qy 1261 GGTCTCAAACTTCTGGCTTCAATCTTCCAAATGAGCCACCAACCCAGCCAGTCA 1320
Db 1261 GGTCTCAAACTTCTGGCTTCAATCTTCCAAATGAGCCACCAACCCAGCCAGTCA 1320
Qy 1321 CATTTTAAACAGTTTACATCTTTTATTTTATAGTATACAGAAAGTAAATACAATAAATGT 1380

Db 1321 CATTTTAAACAGTTTACATCTTTTATTTTATAGTATACAGAAAGTAAATACAATAAATGT 1380
Qy 1381 CAAACCTGCAAAATTCAGTAGTAAACAGAGTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
Db 1381 CAAACCTGCAAAATTCAGTAGTAAACAGAGTCTTTTATTAACCTTTTAAACAAAGCTTTAGAG 1440
Qy 1441 CA 1442
Db 1441 CA 1442

RESULT 7

US-10-092-934-1
; Sequence 1, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)...(1139)
US-10-092-934-1

Query Match 100.0%; Score 1442; DB 14; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTATTTTGTGAGATGGAGTTTTCGCTCTCTGTTGCCCAAGGCTGAGTGCATATGGCGCAA 60
Db 1 TTTTATTTTGTGAGATGGAGTTTTCGCTCTCTGTTGCCCAAGGCTGAGTGCATATGGCGCAA 60
Qy 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGGATTTCTCTGCTCAGCTCCC 120
Db 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGGATTTCTCTGCTCAGCTCCC 120
Qy 121 CAGTAGCTGGGATTTACAGGCAATGTGCACCCACGCTCGGCTAATTTTGTATTTTATTTAG 180
Db 121 CAGTAGCTGGGATTTACAGGCAATGTGCACCCACGCTCGGCTAATTTTGTATTTTATTTAG 180
Qy 181 TAGAGATGGAGTTTCTCATGTTGTGTCAGGCTGCTGAACTCCGACCTCAGATGATC 240
Db 181 TAGAGATGGAGTTTCTCATGTTGTGTCAGGCTGCTGAACTCCGACCTCAGATGATC 240
Qy 241 CCTCGCTCTCGGCTCCCAAGAGTGTAGTACAGGACTGGCCACCATGCCCGGCTCTGCC 300
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Db 301 TGGCTAAATTTTGTGTTAGAAACAGGTTTCACTGATGTGCCCAAGCTGGTCTCTGAGC 360
Qy 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
Db 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTGC 420
Qy 421 CTGGCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
Db 421 CTGGCTTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAG 480
Qy 481 TGCAGTGGTGTATCACAGCTCACTGACGCTTCACTCTGATGTGCCCAAGCTGGTCTCTCTG 540

Db 481 TGCAAGTGGTGTGATCACAGCTCACTGCAGCCTTCAACTCTGAGATCAAGCATCTCTCTG 540
Qy 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGAGATGACCACTACACCTGCGCTAAATTTTA 600
Db 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGAGATGACCACTACACCTGCGCTAAATTTTA 600
Qy 601 TTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCTACCCAGGCTGAGTGCAGT 660
Db 601 TTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCTACCCAGGCTGAGTGCAGT 660
Qy 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCA 720
Db 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCA 720
Qy 721 GCTCTGTAGTAGCTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTTT 780
Db 721 GCTCTGTAGTAGCTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTTT 780
Qy 781 TAGTAGAGATGGGTTCACCATGTTGCGCAGGTGATCTTGATCTCTGGACCTTGTATC 840
Db 781 TAGTAGAGATGGGTTCACCATGTTGCGCAGGTGATCTTGATCTCTGGACCTTGTATC 840
Qy 841 TGCTTGCCTCGGCTCCCAAAAGTGTGGATTACAGGCGTGAGCCACACGCGCGCTTA 900
Db 841 TGCTTGCCTCGGCTCCCAAAAGTGTGGATTACAGGCGTGAGCCACACGCGCGCTTA 900
Qy 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTATACCCAGGCTGAGTGCAT 960
Db 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTATACCCAGGCTGAGTGCAT 960
Qy 961 GCGCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATCTCTCTCTCA 1020
Db 961 GCGCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATCTCTCTCTCA 1020
Qy 1021 GCTTCCCAAGCAGCTGGGATTAAGGCGCACTCGCCACCAACCCCGCTAATTTTGTATTT 1080
Db 1021 GCTTCCCAAGCAGCTGGGATTAAGGCGCACTCGCCACCAACCCCGCTAATTTTGTATTT 1080
Qy 1081 TCATTAGAGCGGGGTTTCCCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGT 1140
Db 1081 TCATTAGAGCGGGGTTTCCCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGT 1140
Qy 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAAGGCGTGAGCCACCTCACCCAG 1200
Db 1141 GACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAAGGCGTGAGCCACCTCACCCAG 1200
Qy 1201 CCGGCTAATTTAGATAAAAAAATATGTAGCAATGGGGGTCTTGCTATGTTGCCAGGCT 1260
Db 1201 CCGGCTAATTTAGATAAAAAAATATGTAGCAATGGGGGTCTTGCTATGTTGCCAGGCT 1260
Qy 1261 GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACCAACCCAGCAGTCA 1320
Db 1261 GGTCTCAAACTTCTGGCTTCATGCAATCCTTCCAAATGAGCCACCAACCCAGCAGTCA 1320
Qy 1321 CATTTTAAACAGTTACATCTTTTATTTAGTATACAGAAAGTAAATACATAAATGT 1380
Db 1321 CATTTTAAACAGTTACATCTTTTATTTAGTATACAGAAAGTAAATACATAAATGT 1380
Qy 1381 CAAACTGCAAAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAG 1440
Db 1381 CAAACTGCAAAATTCAGTAGTAACAGAGTTCTTTTATTAACCTTTTAAACAAAGCTTTAG 1440
Qy 1441 CA 1442
Db 1441 CA 1442

RESULT 8
US-10-153-334-53
; Sequence 53, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)...(1139)
US-10-153-334-53

Query Match 100.0%; Score 1442; DB 14; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTATTTTGTAGATGGAGTTTTCGCTCTGTTGCCAGGCTGGAGTGCATGGCGCA 60
Db 1 TTTTATTTTGTAGATGGAGTTTTCGCTCTGTTGCCAGGCTGGAGTGCATGGCGCA 60
Qy 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCGAAGCGATTCTCTCCCTCAGCTCCC 120
Db 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCGAAGCGATTCTCTCCCTCAGCTCCC 120
Qy 121 CAGTAGCTGGGATTAAGGCGATGTCACCGCTCGGCTAATTTGTATTTTGTATTTT 180
Db 121 CAGTAGCTGGGATTAAGGCGATGTCACCGCTCGGCTAATTTGTATTTTGTATTTT 180
Qy 181 TAGAGATGGAGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
Db 181 TAGAGATGGAGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
Qy 241 CCTCGCTCTCGGCTCCCAAAAGTGTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
Db 241 CCTCGCTCTCGGCTCCCAAAAGTGTAGATACAGGACTGGCCACCATGCCGGCTCTGCC 300
Qy 301 TGGCTAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTGAGC 360
Db 301 TGGCTAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTGAGC 360
Qy 361 TCAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTAAGGCGTGAGCGCGTGC 420
Db 361 TCAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTAAGGCGTGAGCGCGTGC 420
Qy 421 CTGGCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCCACTCTTACCCAGGATGAAG 480
Db 421 CTGGCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCCACTCTTACCCAGGATGAAG 480
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Db 481 TGCAGTGTGTGATCAGAGCTCACTGAGCCTTCAACTCTCTGAGATCAAGCATCTCTG 540
Qy 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGCTAATTTT 600
Db 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGCTAATTTT 600
Qy 601 TTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCTACCCAGGCTGAGTGCAGT 660
Db 601 TTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCTACCCAGGCTGAGTGCAGT 660
Qy 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCA 720
Db 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCA 720
Qy 721 GCCTCTGTAGTAGCTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTTT 780

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721 GCCTCTGAGTAGCTGGGACTACAGGCGCCACACGCGCTAGCTAAATTTTGTATTTT 780
781 TAGTAGAGATGGGGTTTACCAGTCTCGCCAGGTTTGAATCTTGTATCTCTGACCTTGTGATC 840
781 TAGTAGAGATGGGGTTTACCAGTCTCGCCAGGTTTGAATCTTGTATCTCTGACCTTGTGATC 840
841 TGCTCGCTCGGCTCCCCAAGTGTGGGATTAACAGGCGTGAAGCCACCGCCGCTTCA 900
841 TGCTCGCTCGGCTCCCCAAGTGTGGGATTAACAGGCGTGAAGCCACCGCCGCTTCA 900
901 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATACCGAGCTGGAATGCAAT 960
901 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATACCGAGCTGGAATGCAAT 960
961 GGCCTCGCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCA 1020
961 GGCCTCGCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCA 1020
1021 GGCCTCGCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCA 1080
1021 GGCCTCGCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCA 1080
1081 TCAATTAGAGCGGGGTTTACCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
1081 TCAATTAGAGCGGGGTTTACCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
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1141 GACCCACCTCGCTCAGCCTTCCAAAGTGTGGGATTAACAGGCGTGAAGCCACCTCA 1200
1201 CCGGCTAAATTTAGATAAAAAATATAGCAATGGGGGCTCTTGTATGTGCGCAGGCT 1260
1201 CCGGCTAAATTTAGATAAAAAATATAGCAATGGGGGCTCTTGTATGTGCGCAGGCT 1260
1261 GGTCTCAAACTTCTGGCTTCAAGCAATCTTCCAAATGAGCCACCAACACCGCCAGTCA 1320
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1321 CATTTTAAACAGTTACATCTTTATTTAGTATACAGAGTAAATACAAATACATGT 1380
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1381 CAAACCTGCAAAATTCAGTAGTAACAGAGTTCTTTTAACTTTTAAACAAAGCTTTAGAG 1440
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1441 CA 1442
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RESULT 9
 US-10-198-069-48
 ; Sequence 48, Application US/10198069
 ; Publication No. US20030096756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVERBACK, PAUL
 ; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
 ; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
 ; TITLE OF INVENTION: CELLS
 ; FILE REFERENCE: 59003.000009
 ; CURRENT APPLICATION NUMBER: US/10/198,069
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,161
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,150
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: 60/331,477
 ; PRIOR FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 48

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; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-198-069-48

Query Match      100.0%; Score 1442; DB 14; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTTTTCAGATGGAGTTTTCGCTCTTGTGTCGCCAGGCTGAGTGAATGCGCGCAA 60
DB 1 TTTTATTTTTCAGATGGAGTTTTCGCTCTTGTGTCGCCAGGCTGAGTGAATGCGCGCAA 60
QY 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGCTTCAAGCGATTTCTCTGCTCAGCTCCG 120
DB 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGCTTCAAGCGATTTCTCTGCTCAGCTCCG 120
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DB 121 CAGTAGCTGGGATTAACAGGATGTCACCCAGCTCGGCTAAATTTTGTATTTTGTAG 180
QY 181 TAGAGATGGAGTTTCTCCATGTTGTGAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
DB 181 TAGAGATGGAGTTTCTCCATGTTGTGAGGCTGGTCTCGAACTCCGACCTCAGATGATC 240
QY 241 CTTCCGCTCTCGGCTCCCAAGTGTAGATACAGGACTGGGCCACCAATGCCCCGCTCTGCC 300
DB 241 CTTCCGCTCTCGGCTCCCAAGTGTAGATACAGGACTGGGCCACCAATGCCCCGCTCTGCC 300
QY 301 TGGCTAAATTTTGTGTAGAAACAGGTTTCACTGATGTGCCCAAGCTGCTCTCTTGAGC 360
DB 301 TGGCTAAATTTTGTGTAGAAACAGGTTTCACTGATGTGCCCAAGCTGCTCTCTTGAGC 360
QY 361 TCAAGCAGTCCACTGCTCAGCTCCCAAGTGTGGGATTTACAGGCGTGCAGCGCTGC 420
DB 361 TCAAGCAGTCCACTGCTCAGCTCCCAAGTGTGGGATTTACAGGCGTGCAGCGCTGC 420
QY 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
DB 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
QY 481 TGCAGTGTGTGATCAGAGCTCAGTGCAGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
DB 481 TGCAGTGTGTGATCAGAGCTCAGTGCAGCTTCAACTCTCTGAGATCAAGCATCTCTCTG 540
QY 541 CTTCAGCTCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGCTAAATTTT 600
DB 541 CTTCAGCTCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGCTAAATTTT 600
QY 601 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
DB 601 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
QY 661 GCGCAATCTTGGCTCAGTGCAGCTTCTGCTCCCGGTTCAAGTTATTTCTCTGCGCCA 720
DB 661 GCGCAATCTTGGCTCAGTGCAGCTTCTGCTCCCGGTTCAAGTTATTTCTCTGCGCCA 720
QY 721 GCCTCTCAGTAGCTGGGACTACAGGCGCCCAACAGCTAGCTAAATTTTGTATTTT 780
DB 721 GCCTCTCAGTAGCTGGGACTACAGGCGCCCAACAGCTAGCTAAATTTTGTATTTT 780
QY 781 TAGTAGAGATGGGGTTTACCATGTTTGGCAGGTTGATCTTGTATCTCTGAGCTTGTGATC 840
DB 781 TAGTAGAGATGGGGTTTACCATGTTTGGCAGGTTGATCTTGTATCTCTGAGCTTGTGATC 840
QY 841 TGCCTGCTCGGCTCCCAAGTGTGGGATTTACAGGCGTGAAGCCACCGCCGCTTCA 900
DB 841 TGCCTGCTCGGCTCCCAAGTGTGGGATTTACAGGCGTGAAGCCACCGCCGCTTCA 900
QY 901 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTATACCGAGCTGGAATGCAAT 960

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Db 901 TTTTAAATTTTGTGTTGAAATGAAATCTCACTCTGTTACCCAGGCTGGAGTGCAAT 960
Qy 961 GGCCTCAATCTCGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCTCTGTCTCA 1020
Db 961 GGCCTCAATCTCGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCTCTGTCTCA 1020
Qy 1021 GCTTCCCAAGCAGCTGGGATTACGGGCACCTGCGCACCAACCCCGCTAAATTTTGTATTT 1080
Db 1021 GCTTCCCAAGCAGCTGGGATTACGGGCACCTGCGCACCAACCCCGCTAAATTTTGTATTT 1080
Qy 1081 TCATTAGAGCGCGGGTTTCACCATATTTCTCAGGCTGGTCTCAAACTCTCTGACCTCAGT 1140
Db 1081 TCATTAGAGCGCGGGTTTCACCATATTTCTCAGGCTGGTCTCAAACTCTCTGACCTCAGT 1140
Qy 1141 GACCCACCTGCTCAGCTTCCAAAGTGTGGGATTACAGGGGTGAGCCACCTCACCCAG 1200
Db 1141 GACCCACCTGCTCAGCTTCCAAAGTGTGGGATTACAGGGGTGAGCCACCTCACCCAG 1200
Qy 1201 CCGGCTAAATTTAGATAAATAATGTAGCAATGGGGGTCTTGCTATGTTGCCAGGCT 1260
Db 1201 CCGGCTAAATTTAGATAAATAATGTAGCAATGGGGGTCTTGCTATGTTGCCAGGCT 1260
Qy 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACCAACCCAGCGTCA 1320
Db 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCACCAACCCAGCGTCA 1320
Qy 1321 CATTTTAAACAGTTACATCTTTATTTTGTAGTATCTAGAAAGTAAATCAATAAACAATG 1380
Db 1321 CATTTTAAACAGTTACATCTTTATTTTGTAGTATCTAGAAAGTAAATCAATAAACAATG 1380
Qy 1381 CAACTGCAAAATTCAGTAGTACAGAGTTCTTTTATACCTTTTAAACAGCTTTAGAG 1440
Db 1381 CAACTGCAAAATTCAGTAGTACAGAGTTCTTTTATACCTTTTAAACAGCTTTAGAG 1440
Qy 1441 CA 1442
Db 1441 CA 1442

RESULT 10
US-10-198-070-125
; Sequence 125, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-198-070-125
Query Match 100.0%; Score 1442; DB 15; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTAAATTTTGTGAGATGAGATTTTGGCTCTCTGTTGCCCCAGGCTGAGTGCAATGGCGAA 60
Db 1 TTTTAAATTTTGTGAGATGAGATTTTGGCTCTCTGTTGCCCCAGGCTGAGTGCAATGGCGAA 60
Qy 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCC 120
Db 61 TCTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCC 120
Qy 121 CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTGTAG 180
Db 121 CAGTAGCTGGGATTACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTGTAG 180
Qy 181 TAGAGATGGAGTTTCTCAGTTGTGTGCTAGGCTGGTCTGAACTCCGACCTCAGATGATC 240
Db 181 TAGAGATGGAGTTTCTCAGTTGTGTGCTAGGCTGGTCTGAACTCCGACCTCAGATGATC 240
Qy 241 CCTCCGCTCCGCTCCCAAAAGTGTAGATACAGGACTGGCCACCATGCCCGGCTCTGCC 300
Db 241 CCTCCGCTCCGCTCCCAAAAGTGTAGATACAGGACTGGCCACCATGCCCGGCTCTGCC 300
Qy 301 TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAAGCTGGTCTCCTGAGC 360
Db 301 TGGCTAAATTTTGTGTAGAAACAGGGTTTCACTGATGTGCCAAAGCTGGTCTCCTGAGC 360
Qy 361 TCAAGCAGTCCACCTGCTCAGCTCCCAAAAGTGTGGGATTACAGGGGTGCGAGCGTGC 420
Db 361 TCAAGCAGTCCACCTGCTCAGCTCCCAAAAGTGTGGGATTACAGGGGTGCGAGCGTGC 420
Qy 421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCTTACCCAGGATGAAG 480
Db 421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCTTACCCAGGATGAAG 480
Qy 481 TGCAGTGTGTGATCAGAGCTCACTGAGCCCTTCAACTCTTGAGATCAAGCATCTCCTG 540
Db 481 TGCAGTGTGTGATCAGAGCTCACTGAGCCCTTCAACTCTTGAGATCAAGCATCTCCTG 540
Qy 541 CCTCAGCTCCCAAGTAGCTGGGACCAAGACATGCACTACCTGGGCTAAATTTT 600
Db 541 CCTCAGCTCCCAAGTAGCTGGGACCAAGACATGCACTACCTGGGCTAAATTTT 600
Qy 601 TTTTAAATTTTAAATTTTGTGAGACAGATCTCAACTGTGTCCACAGGCTGGAGTGCAAT 660
Db 601 TTTTAAATTTTAAATTTTGTGAGACAGATCTCAACTGTGTCCACAGGCTGGAGTGCAAT 660
Qy 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCA 720
Db 661 GCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCA 720
Qy 721 GCCTCTGAGTAGCTGGGACTACAGGCGCCCACTGCTGCTCCCGGGTTCAAGTTATTT 780
Db 721 GCCTCTGAGTAGCTGGGACTACAGGCGCCCACTGCTGCTCCCGGGTTCAAGTTATTT 780
Qy 781 TAGTAGAGATGGGGTTTCAACATGTTTCGCGAGGTGATCTTGATCTCTGAGACCTCTGATC 840
Db 781 TAGTAGAGATGGGGTTTCAACATGTTTCGCGAGGTGATCTTGATCTCTGAGACCTCTGATC 840
Qy 841 TGCTTGCCTCGGCTCCCAAAAGTGTGGGATTACAGGGGTGAGCCACCAACCCCGGCTTA 900
Db 841 TGCTTGCCTCGGCTCCCAAAAGTGTGGGATTACAGGGGTGAGCCACCAACCCCGGCTTA 900
Qy 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTGTGTACCCAGGCTGGAGTGCAAT 960
Db 901 TTTTAAATTTTGTGTTGAAATGGAATCTCACTGTGTACCCAGGCTGGAGTGCAAT 960
Qy 961 GGCCTCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCTCTGTCTCA 1020
Db 961 GGCCTCAATCTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCTCTGTCTCA 1020
Qy 1021 GCCTCCCAAGCAGCTGGGATTACGGGCACCTGCGCACCAACCCCGCTAAATTTTGTATTT 1080
Db 1021 GCCTCCCAAGCAGCTGGGATTACGGGCACCTGCGCACCAACCCCGCTAAATTTTGTATTT 1080

Db 1321 CATTTTAAACAGTTACATCTTTATTTTGTATATACTAGAAAGTAATACAATAAACATGT 1380
QY 1381 CAAACCTGCAAAATTCAGTAGTAACAGAGTTCTTTTATAACTTTTAAACAAAGCTTTAGAG 1440
Db 1381 CAAACCTGCAAAATTCAGTAGTAACAGAGTTCTTTTATAACTTTTAAACAAAGCTTTAGAG 1440
QY 1441 CA 1442
Db 1441 CA 1442

RESULT 12

US-10-910-173-1
; Sequence 1, Application US/10910173
; Publication No. US20050090441A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/10/910,173
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/872,968
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-910-173-1

Query Match 100.0%; Score 1442; DB 21; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTTTTCAGATGGAGTTTCGCTCTGTGCCCCAGGCTGGAGTGCATGGCGCAA 60
Db 1 TTTTATTTTTCAGATGGAGTTTCGCTCTGTGCCCCAGGCTGGAGTGCATGGCGCAA 60
QY 61 TCTAGCTCACCGCAACTCCGCCCTCCGGGTTTCAAGGATTTCTCTGCTCAGCTCCC 120
Db 61 TCTAGCTCACCGCAACTCCGCCCTCCGGGTTTCAAGGATTTCTCTGCTCAGCTCCC 120
QY 121 CAGTAGCTGGGATTAACGATGATGACCCAGCTCGGCTAAATTTGTATTTTTTTAG 180
Db 121 CAGTAGCTGGGATTAACGATGATGACCCAGCTCGGCTAAATTTGTATTTTTTTAG 180
QY 181 TAGAGATGGAGTTTCTCCATGTTGGTTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
Db 181 TAGAGATGGAGTTTCTCCATGTTGGTTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 240
QY 241 CTTCCGCTCTCGGCCCTCCCAAAGTGTAGATACAGACTGGCCACCATGCGCGCTCTGCC 300
Db 241 CTTCCGCTCTCGGCCCTCCCAAAGTGTAGATACAGACTGGCCACCATGCGCGCTCTGCC 300
QY 301 TGGCTAAATTTTGTGGTAGAAACAGGTTTCACTGATGTCGCAAGCTGGTCTCTGAGC 360
Db 301 TGGCTAAATTTTGTGGTAGAAACAGGTTTCACTGATGTCGCAAGCTGGTCTCTGAGC 360
QY 361 TCAAGCAGTCCACCTCGCCTCAGCCTCCCAAAGTGTGGGATTAACAGGCGTGCAGCGTGC 420
Db 361 TCAAGCAGTCCACCTCGCCTCAGCCTCCCAAAGTGTGGGATTAACAGGCGTGCAGCGTGC 420
QY 421 CTGGCTTTTATTTTATTTTATTTTAAACAGAGTGTCCCACTCTTACCCAGGATGAAG 480
Db 421 CTGGCTTTTATTTTATTTTATTTTAAAGACACAGGTTGCCACTCTTACCCAGGATGAAG 480
QY 481 TGCAGTGTGTGATCACAGCTCACCTGAGCCTTCACTCTGAGATCAAGCATCTCTCTG 540
Db 481 TGCAGTGTGTGATCACAGCTCACCTGAGCCTTCACTCTGAGATCAAGCATCTCTCTG 540
QY 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGGCTTAATTTTAA 600

Db 541 CCTCAGCCTCCCAAGTAGCTGGGACCAAGACATGCACCATACCTGGGCTTAATTTTAA 600
QY 601 TTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCAGCTGGAGTGCAGT 660
Db 601 TTTTATTTTAAATTTTGTGAGACAGAGTCTCAACTCTGTCAACCAGCTGGAGTGCAGT 660
QY 661 GGGCGAATCTTGGGCTCACTGCAACCTCTGCTCCGGGTTCAAGTTATCTCTCTGCCCA 720
Db 661 GGGCGAATCTTGGGCTCACTGCAACCTCTGCTCCGGGTTCAAGTTATCTCTCTGCCCA 720
QY 721 GCCTCCTCAGTAGCTGGGACTACAGGCGCCCAACACGCTAGCTAATTTTGTATTTT 780
Db 721 GCCTCCTCAGTAGCTGGGACTACAGGCGCCCAACACGCTAGCTAATTTTGTATTTT 780
QY 781 TAGTAGAGATGGGTTTCAACATGTTTCGACAGTTGATCTTGATCTCTCGAAGCTTGTGATC 840
Db 781 TAGTAGAGATGGGTTTCAACATGTTTCGACAGTTGATCTTGATCTCTCGAAGCTTGTGATC 840
QY 841 TGCCTGCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGCCACACCGCCGGCTTA 900
Db 841 TGCCTGCTCGGCTCCCAAGTGTGGGATTAACAGGCTGAGCCACACCGCCGGCTTA 900
QY 901 TTTTATTTTGTGTTTGAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAT 960
Db 901 TTTTATTTTGTGTTTGAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAT 960
QY 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCGGGCTCAAGCGATCTCTCTCTCA 1020
Db 961 GGCCAAATCTCGGCTCACTGCAACCTCTGCTCCGGGCTCAAGCGATCTCTCTCTCA 1020
QY 1021 GCCTCCCAAGCAGCTGGGATTAACGGGCACTGCGCACCAACACCGCTAAATTTGTATTT 1080
Db 1021 GCCTCCCAAGCAGCTGGGATTAACGGGCACTGCGCACCAACACCGCTAAATTTGTATTT 1080
QY 1081 TCATTAGAGGCGGGTTTCAACATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
Db 1081 TCATTAGAGGCGGGTTTCAACATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGGT 1140
QY 1141 GACCCACCTGCTCAGCCTTCAAAGTGTGGGATTAACAGGCTGAGCCACCTCAACCAG 1200
Db 1141 GACCCACCTGCTCAGCCTTCAAAGTGTGGGATTAACAGGCTGAGCCACCTCAACCAG 1200
QY 1201 CCGGCTAATTTAGATAAAAAATATGTAGCAATGGGGGCTCTGCTATGTGCCCCAGCT 1260
Db 1201 CCGGCTAATTTAGATAAAAAATATGTAGCAATGGGGGCTCTGCTATGTGCCCCAGCT 1260
QY 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCCAACACCCAGCCAGTCA 1320
Db 1261 GGTCTCAAACTTCTGGCTTCATGCAATCTTCCAAATGAGCCCAACACCCAGCCAGTCA 1320
QY 1321 CATTTTAAACAGTTATCATCTTTTATTTAGTATCTAGAAAGTAAATCAATAAATGT 1380
Db 1321 CATTTTAAACAGTTATCATCTTTTATTTAGTATCTAGAAAGTAAATCAATAAATGT 1380
QY 1381 CAAACCTGCAAAATTCAGTAGTAACAGAGTTCTTTTATAACTTTTAAACAAAGCTTTAG 1440
Db 1381 CAAACCTGCAAAATTCAGTAGTAACAGAGTTCTTTTATAACTTTTAAACAAAGCTTTAG 1440
QY 1441 CA 1442
Db 1441 CA 1442

RESULT 13

US-09-964-666-4
; Sequence 4, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: US/09/964,666
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Emond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-964-666-4

Query Match 84.8%; Score 1223.4; DB 9; Length 1418;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

QY 2 TTTTCTTTTGTAGATGGAGTTTCTGCTGTTGCTCCAGGCTGGAGTGCATGGCGCAAT 61
DB 1 TTTTCTTTTGTAGATGGAGTTTCTGCTGTTGCTCCAGGCTGGAGTGCATGGCGCAAT 60

QY 62 CTCAGCTCACCGCAACCTCCGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 121
DB 61 CTCAGCTCACCGCAACCTCCGCTCCCGGTTCAAGCGATTCTCTGCTCAGCCTCCCC 120

QY 122 AGTA-GCTGGGATACAGCATGTGCACCGCTCGGCTAATTTTGTATTTTGTAG 180
DB 121 AGTAGGCTGGGATACAGGCATGTGCA-CCAGCTCGGCTAATTTTGTATTTTGTAG 179

QY 181 TAGAGATGGAGTTTCTCCATGTTGTTGCTAGGCTGTTCTGAACTCCCGACCTCAGATGATC 240
DB 180 TAGAGATGGAGTTTCTCCATGTTGTTGCTAGGCTGTTCTGAACT-CCGACCTCAGATGATC 238

QY 241 CTCGCTCTCGGCTCTCCAAAGTGTAGATACAGGCTGGCCACCATGCGCGG-CTCTGC 299
DB 239 CTCGCTCTCGGCTCTCCAAAGTGTAGATACAGGCTGGCCACCATGCGCGCTCTGC 298

QY 300 CTGGCTAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGTCTCTGAG 359
DB 299 CTGGCTAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGTCTCTGAG 358

QY 360 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGATACAGGGTGCAGCGCTG 419
DB 359 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGATACAGGGTGCAGCGCTG 418

QY 420 CTGGCTCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGATGAA 479
DB 419 CTGGCTCTTTTATTTTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGATGAA 478

QY 480 GTGAGTGGTGTGATCAAGCTCACTGAGGCTTCACTCTGAGATCAAGCATCTCTCT 539

DB 479 GTGAGTGGTGTGATCAAGCTCACTGAGCCTTCAACT-CTGAGATCAAGCATCTCTCT 537
QY 540 GCTCAGAGCTCC-AGTAGCTGGGACCAAGACATGACCACTACACTCTGCTGCTAATTTT 598
DB 538 GCTCAGAGCTCCAAAGTAGCTGGGACCAAGACATGACCACTACACTCTGCTAATTTT 597
QY 599 TATTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGA 658
DB 598 TATTTTATTTTAAATTTTGTAGACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGA 657
QY 659 GTGGCGCATCTTGGCTCACTGCAACCTCTGCTCCGGGTTCAAGTATTTCTCTGCGCC 718
DB 658 GTGGCGCATCTTGGCTCACTGCAACCTCTGCTCCGGGTTCAAGTATTTCTCTGCGCC 717
QY 719 CAGCCTCTGAGTAGCTGGGACTACAGCGCCCAACAGCTAGCTAAATTTTGTATTT 778
DB 718 CAGCCTCTGAGTAGCTGGGACTACAGCGCCCAACAGCTAGCTAAATTTTGTATTT 777
QY 779 TTTAGTAGAGTGGG-TTCAACCATGTTGCGCAGGTTGAT-CTTGATCTCTGAGCCTTGT 836
DB 778 TTTAGTAGAGTGGGTTTCAACCATGTTGCGCAGGTTGATCTAGATCTCTTGACCTGT 837
QY 837 GATCTGCTGCTCGGCTCCCAAGTGTCTGGGATTAAGG-CGTGAGGCACACGCCCG 895
DB 838 GATCTGCTGCTCGGCTCCCAAGTGTCTGGGATTAAGGACGTGACGCCCAACGCCCG 897
QY 896 GCTTATTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGCTTACCCAGGCTGGAGT 955
DB 898 GCTTATTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTTACCCAGGCTGGAGT 957
QY 956 GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTCTCTCTG 1015
DB 958 GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATTCTCTCTG 1017
QY 1016 TCTCAGCTCCCAAGCAGCTGGGATTAAGGCACTGCTGCTCCCGGCTCAAGCGATTCTCTCTG 1075
DB 1018 TCTCAGCTCCCAAGCAGCTGGGATTAAGGCACTGCTGCTCCCGGCTCAAGCGATTCTCTCTG 1076
QY 1076 TATTTTCAATTAAGCGGGGTTTCAACCATATTTGTCAGGCTGCTCAAACTCTGACCT 1135
DB 1077 TATTTTCAATTAAGCGGGGTTTCAACCATATTTGTCAGGCTGCTCAAACTCTGACCT 1136
QY 1136 CAGTGACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAAGGCGTGAGCCACCTCA 1195
DB 1137 CAGTGACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTAAGGCGTGA--CGCCTCA 1194
QY 1196 CCGAGCGGCTAATTTAGATATAAATAATATGAGCAATGGGGGCTTCTGCTATGTTGCC 1255
DB 1195 CCGAGCGGCTAATTTAGATATAAATAATATGAGCAATGGGGGCTTCTGCTATGTTGCC 1254
QY 1256 AGGCTGCTCAAACTCTGCTCATGCAATCTTCCAAATGAGCCACCAACCCAGCC 1315
DB 1255 AGGCTGCTCAAACTCTGCTCATGCAATCTTCCAAATGAGCCACCAACCCAGCC 1314
QY 1316 AGTCACATTTTAAACAGTATACATCTTTATTTAGTATCTAGAAAGTAAATCAATAA 1375
DB 1315 AGTCACA-TTTTAAACAGTATACATCTTTATTTAGTATCTAGAAAGTATACATAA 1373
QY 1376 CATGTCAAACTGCAATTCAGTAGTAGTAAACAGATTTCTTT 1414
DB 1374 ATGGCGAACCCTGCAATTCGAGTAGTAGTAAACAGATTTCTTT 1412

RESULT 14
US-09-964-412-4
; Sequence 4, Application US/09964412
; Patent No. US2002012931A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease

; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/964,412
 ; FILING DATE: 28-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 0609.4370000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1418 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-964-412-4

Query Match	84.8%	Score 1223.4	DB 9	Length 1418
Best Local Similarity	96.9%	Pred. No. 0		
Matches 1375	Conservative 0	Mismatches 31	Indels 13	Gaps 12

Qy	2	TTTTTTTTTTGAGATGGAGTTTTGCGTCTGTGTGCCCAGGCTGGAGTGCATGGCGCAAT	61
Db	1	TTTTTTTTTTGAGATGGAGTTTTGCGTCTGTGTGCCCAGGCTGGAGTGCATGGCGCAAT	60
Qy	62	CTCAGCTCACCGCAACCTCCGCGCTCCCGGGTCTAAAGCGATTCTCTCGCTCAGCCTCCCC	121
Db	61	CTCAGCTCACCGCAACCTCCGCGCTCCCGGGTCTAAGCGATTCTCTCGCTCAGCCTCCCC	120
Qy	122	AGTA-GCTGGGATTACAGGATGTGCACCAACGCTCGGCTAAATTTGTATTTTTTTTATG	180
Db	121	AGTAGGCTGGGATTTACAGGCATGTGCA-CCACGCTCGGCTAAATTTGTATTTTTTTTATG	179
Qy	181	TAGAGATGGAGTTCTCCATGTGGTTCAGGCTGGTCTCGAACTCCCGAACCTCAGATGATC	240
Db	180	TAGAGATGGAGTTCTCCATGTGGTTCAGGCTGGTCTCGAACT-CCGACCTCAGATGATC	238
Qy	241	CCTCCGCTCTCGGCTCCCAAAGTGCTAGATACAGGACTGGCGCACCATGCCCG-CTCTGC	299
Db	239	CTCCGCTCTCGGCTCCCAAAGTGCTAGATACAGGACTTGAGCACCATGCCCGGCTCTGC	298
Qy	300	CTGGCTAAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTGTAG	359
Db	299	CTGGCTAAATTTTGTGGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTGTAG	358
Qy	360	CTCAAGCAGTCCACCTGCGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTG	419
Db	359	CTCAAGCAGTCCACCTGCGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCGTGCAGCGGTG	418
Qy	420	CCTGGCCTTTTATTTTTTATTTTTTAAAGACACAGGTGTGCCACTCTTACCCAGGATGAA	479
Db	419	CCTGGCCTTTTATTTTTTATTTTTTAAAGACACAGGTGTGCCACTCTTACCCAGGATGAA	478
Qy	480	GTGCAGTGGTGTGATNCACAGCTACCTGACGCTTCAACTCCTGAGATCAAGCATCTCTCT	539
Db	479	GTGCAGTGGTGTGATNCACAGCTACCTGACGCTTCAACT-CTGAGATCAAGCATCTCTCT	537

QY	540	GCCTCAGCCTCCC--AAGTAGCTGGGACCAAGAAGATGCACCACTACACCTGGCTAATTTT	598
DB	538	GCCTCAGCCTCCCAGAAAGTAGCTGGGACCAAGAAGATGCACCACTACACCTGGCTAATTTT	597
QY	599	TATTTTATTTTAAATTTTGAAGCAGAGTCTCAACTCTGTCAACCGCTGGAGTGCA	658
DB	598	TATTTTATTTTAAATTTTGAAGCAGAGTCTCAACTCTGTCAACCGCTGGAGTGCA	657
QY	659	GTGGCGCAATCTTGGCTCACTGCAACCTTGCCTCCCGGGTTCAAGTTATTCTCTGGCC	718
DB	658	GTGGCGCAATCTTGGCTCACTGCAACCTTGCCTCCCGGGTTCAAGTTATTCTCTGGCC	717
QY	719	CAGCCTCTCTGATGAGCTGGGACTACAGCGCCCAACCAAGCTAGCTAAATTTTTTGTATT	778
DB	718	CAGCCTCTCTGATGAGCTGGGACTACAGCGCCCAACCAAGCTAGCTAAATTTTTTGTATT	777
QY	779	TTTAGTAGAGATGGG--TTCAACCATGTCGCCAGGTTGAT--CTTGATCTCTGGACCTTGT	836
DB	778	TTTAGTAGAGATGGGTTTCAACCATGTCGCCAGGTTGATGCTAGATCTCTTTGACCTTGT	837
QY	837	GATCTGCTGCTCGGCCCTCCAAAGTGCTCGGGAATTACAG--CGTAGCCCAACCAAGCCG	895
DB	838	GATCTGCTGCTCGGCCCTCCAAAGTGCTCGGGAATTACAGGACGTGACGCCACCGCCG	897
QY	896	GCTTATTTTAAATTTTGTGTTGTTGAAATGGAATCTCACTCTGTACCAAGCTGGAGT	955
DB	898	GCCTATTTTAAATTTTGTGTTGTTGAAATGGAATCTCACTCTGTACCAAGCTGGAGT	957
QY	956	GCAATGGCCAAATCTGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTTCTCTG	1015
DB	958	GCAATGGCCAAATCTGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTTCTCCTG	1011
QY	1016	TCTCAGCTCCCAAGCAGCTGGGATTACGGGCACTGCGCACCAACCCCGCTAATTTTGG	1075
DB	1018	TCTCAGCTCCCAAGCAGCTGGGATTACGGGCACTGCGCACCACTG--CACCAACCCCGTAA	1077
QY	1076	TATTTTCATTAGAGCGGGGTTTCAACCATTTTGTCAAGCTGGTCTCAAACTCTCGACT	1133
DB	1077	TATTTTCATTAGAGCGGGGTTTCAACCATTTTGTCAAGCTGGTCTCAAACTCTCGACT	1133
QY	1136	CAGGTGACCCACCTGCTCAGCTTCCAAAGTGCTGGGATTACAGGCGTAGCCACCTCA	1199
DB	1137	CAGGTGACCCACCTGCTCAGCTTCCAAAGTGCTGGGATTACAGGCGTGA--CGCTCA	1199
QY	1196	CCGAGCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGCTTGTCTATGTTGCC	1255
DB	1195	CCGAGCGGCTAAATTTAGATAAAAAATATGTAGCAATGGGGGCTTGTCTATGTTGCC	1255
QY	1256	AGGCTGGTCTCAAACTCTGCTTTCATGCAATCTTCCAAATGAGCCACAACCCAGCC	1315
DB	1255	AGGCTGGTCTCAAACTCTGCTTTCATGCAATCTTCCAAATGAGCCACAACCCAGCC	1311
QY	1316	AGTCACATTTTTTAAACAGTTTACATCTTTATTTTAGTATATACTAGAAAGTAATAAATAA	1375
DB	1315	AGTCACA--TTTTTAAACAGTTTACATCTTTATTTTAGTATATACTAGAAAGTGATACGATAAC	1375
QY	1376	CATGTCAAACTGCAAAATTCATGATAGTAAACAGAGTCTTTT	1414
DB	1374	ATGGCGGAACCTGCAAAATTCATGATAGTAAACAGAGTCTTTT	1412

RESULT 15
US-09-964-667-4
; Sequence 4, Application US/09964667
; Publication No. US20030033621A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/964,667
 FILING DATE: 28-Sep-2001
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0609,4370000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1418 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-964-667-4

Query Match 84.8%; Score 1223.4; DB 10; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

QY	2	TTTTTTTTTTGAGATGGAGTTTTCGCTCTGTGTTGCCAGGCTGGAGTGCATGGCGCAAT	61
DB	1	TTTTTTTTTTGAGATGGAGTTTTCGCTCTGTGTTGCCAGGCTGGAGTGCATGGCGCAAT	60
QY	62	CTCAGCTACCGCAACTCCGGCTCCCGGGTTCAAGCGATTCTCTGCTCCAGCCTCCCC	121
DB	61	CTCAGCTACCGCAACTCCGGCTCCCGGGTTCAAGCGATTCTCTGCTCCAGCCTCCCC	120
QY	122	AGTA-GCTGGATTACAGGATGTGCAACCCAGCTCCGCTAAATTTGTTATTTTATTTAG	180
DB	121	AGTAGGCTGGGATTACAGGATGTGCA-CCAGCTCGGCTAAATTTGTTATTTTATTTAG	179
QY	181	TAGAGATGAGTTTCTCCATGTTGTTGAGGCTGTTCCGAATCCCGACCTCAGATGATC	240
DB	180	TAGAGATGAGTTTCTCCATGTTGTTGAGGCTGTTCCGAATCCCGACCTCAGATGATC	238
QY	241	CCTCGCTCTCGGCTCCCAAGTGTAGATACAGGATGCGGCCACCAATGCCCGG-CTCTGC	299
DB	239	CTCCGCTCTCGGCTCCCAAGTGTAGATACAGGATGCGGCCACCAATGCCCGGCTCTGC	298
QY	300	CTGGCTAAATTTTGGTGAAGAACAGGGTTTCACTGATGCGCCAGCTGGTCTCCTGAG	359
DB	299	CTGGCTAAATTTTGGTGAAGAACAGGGTTTCACTGATGCGCCAGCTGGTCTCCTGAG	358
QY	360	CTCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTACAGGCGTGCAGCCGTG	419
DB	359	CTCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTACAGGCGTGCAGCCGTG	418
QY	420	CCTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	479
DB	419	CCTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	478
QY	480	GTGAGTGTGTGATCACAGCTCACTGAGGCTTCAACTCTCTGAGATCAAGCATCTCTCT	539
DB	479	GTGAGTGTGTGATCACAGCTCACTGAGGCTTCAACT-CTGAGATCAAGCATCTCTCTCT	537

QY	540	GCCTCAGCTCC-AAGTAGCTGGACCAAAACATGACACCTACACCTGGCTAATTTT	598
DB	538	GCCTCAGCTCCCAAGTAGCTGGACCAAAACATGACACCTACACCTGGCTAATTTT	597
QY	599	TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	658
DB	598	TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	657
QY	659	GTGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTTCTCTGCC	718
DB	658	GTGGCGCAATCTTGGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTTCTCTGCC	717
QY	719	CAGCCTCTCTGAGTAGCTGGGACTACAGGCGCCACACAGCCTAGCTAAATTTTCTAT	778
DB	718	CAGCCTCTCTGAGTAGCTGGGACTACAGGCGCCACACAGCCTAGCTAAATTTTCTAT	777
QY	779	TTTAGTAGAGATGGGG-TTCACCATGTTGCGCCAGGTTGAT-CTTGATCTCTGACCTTGT	836
DB	778	TTTAGTAGAGATGGGGTTTCAACATGTTGCGCCAGGTTGATGCTAGATCTCTTGACCTTGT	837
QY	837	GATCTGCTGCTCGGCTCCCAAGTGTCTGGGATTACAGG-CETGAGCCACACCCCG	895
DB	838	GATCTGCTGCTCGGCTCCCAAGTGTCTGGGATTACAGGAGCGTGCACCCACCCCG	897
QY	896	GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	955
DB	898	GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	957
QY	956	GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGTCAAGGATTTCTCTG	1015
DB	958	GCAATGGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGGTCAAGGATTTCTCTG	1017
QY	1016	TCTCAGCCTCCCAAGCAGCTGGGATTACGGGCACTGCGCCACCAACCCCGCTAAATTTT	1075
DB	1018	TCTCAGCCTCCCAAGCAGCTGGGATTACGGGCACTG-CACCACACCCCGCTAAATTTT	1076
QY	1076	TATTTTATTTTATTTAGGCGGGGTTTCAACATATTTTGTGAGGCTGGTCTCAAACTCTGACCT	1135
DB	1077	TATTTTATTTTATTTAGGCGGGGTTTCAACATATTTTGTGAGGCTGGTCTCAAACTCTGACCT	1136
QY	1136	CAGGTGACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTACAGGCTGAGCCACTCA	1195
DB	1137	CAGGTGACCCACCTGCTCAGCCTTCCAAAGTGTGGGATTACAGGCTGAG--CGCCTCA	1194
QY	1196	CCAGCGGCTAAATTTAGATAAAATATATGCAATGGGGGCTTGTCTATGTTGCC	1255
DB	1195	CCAGCGGCTAAATTTAGATAAAATATATGCAATGGGGGCTTGTCTATGTTGCC	1254
QY	1256	AGGCTGGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCC	1315
DB	1255	AGGCTGGTCTCAAACTTCTGGCTTCAATGCAATCTTCCAAATGAGCCACCAACCCAGCC	1314
QY	1316	AGTCAATTTTATTTTAAACAGTTACATCTTTATTTTATTTTATTTTATTTTATTTTATTTT	1375
DB	1315	AGTCAATTTTATTTTAAACAGTTACATCTTTATTTTATTTTATTTTATTTTATTTTATTTT	1373
QY	1376	CATGTCAAACTGCAAAATTCAGTAGTAACAGAGTTCTTT	1414
DB	1374	ATGGCGGAACCTTGCAAAATTCGAGTAGTAGACAGAGTTCTTT	1412

Search completed: September 15, 2005, 22:16:25
 Job time : 1054 sec

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2005, 19:28:46 ; Search time 18 Seconds
(without alignments)
2004.516 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLLPRLCNGAISAH.....FIRGGVSPYLGSWQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	382.5	18.8	673	F40201	artifact-warning s
2	315.5	15.5	613	C40201	artifact-warning s
3	315.5	15.5	627	A40201	artifact-warning s
4	291.5	14.3	597	E40201	artifact-warning s
5	197.5	9.7	579	D40201	artifact-warning s
6	175	8.6	499	S65657	alpha-1C-adrenergi
7	167	8.2	46	I54375	gene NP2 protein -
8	161	7.9	841	I78885	serine/threonine-s
9	157	7.7	39	I54374	gene NF2 protein -
10	151.5	7.4	301	A40201	artifact-warning s
11	139.5	6.9	100	A46010	X-linked retinopat
12	137.5	6.8	79	A56194	thromboxane A-2 re
13	137.5	6.8	407	T02670	probable thromboxa
14	128	6.3	53	A42442	integrin beta-1 ch
15	112	5.5	440	A26359	decay-accelerating
16	106.5	5.2	1125	T19193	hypothetical prote
17	105	5.2	522	T08711	gamma-adaptin homo
18	102.5	5.0	331	S59501	interferon recepto
19	99.5	4.9	331	A54295	interferon alpha/b
20	96.5	4.7	1643	1 RRGNV	genome polypeptin
21	96	4.7	458	E82175	conserved hypothet
22	92	4.5	964	T15342	hypothetical prote
23	91.5	4.5	542	S39608	transcription fact
24	91.5	4.5	631	A36749	genome polypeptin
25	91.5	4.5	1776	1 RRPYM	middle surface ant
26	90.5	4.4	282	1 SAVL64	DNA-directed DNA p
27	90.5	4.4	832	1 S20752	large surface anti
28	90	4.4	431	1 SAVLC2	probable xylogluca
29	89	4.4	299	2 F84785	

30	89	4.4	333	2 AI2131	hypothetical prote
31	89	4.4	1162	2 B97852	hypothetical prote
32	88	4.3	209	2 JC4244	heat-shock 27k pro
33	88	4.3	726	2 S18208	rabphilin-3A-inter
34	88	4.3	832	2 S71785	DNA-directed DNA p
35	87.5	4.3	494	2 S39607	transcription fact
36	87	4.3	226	1 JQ1574	major surface anti
37	87	4.3	226	2 JQ1574	surface antigen -
38	87	4.3	470	2 T05258	glycine hydroxymet
39	87	4.3	1153	2 A49676	nitric-oxide synth
40	86.5	4.3	360	2 T45956	hypothetical prote
41	86.5	4.3	1886	2 S04921	nuclear pore prote
42	86	4.2	262	2 AF2291	hypothetical prote
43	86	4.2	625	2 E96721	hypothetical prote
44	85.5	4.2	832	1 JQVLA1	DNA-directed DNA p
45	84.5	4.2	191	2 C72455	hypothetical prote

ALIGNMENTS

RESULT 1

F40201
artifact-warning sequence (translated ALU class F) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: F40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: F40201
A:Molecule type: DNA
A:Residues: 1-673 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of t

Query Match	18.8%	Score 382.5;	DB 4;	Length 673;
Best Local Similarity	33.2%	Pred No. 6.4e-26;		
Matches 128;	Conservative 19;	Mismatches 111;	Indels 127;	Gaps 17;
QY	16	ISAHNRRLPGSSDPSASPVAGITGCTHARLILYFPLVEMEFHVGQAGLELPTSD	75	
Db	371	VLACHSLNLGSSDPSASVSRVAGITGMRHSLI-YVFLIETQPHVDQAGLKLTSSD	429	
QY	76	PSVSASQARVYRTGTHARLCLANFCGRNVRVSLMCPSSPE-LKQSTCLSLPKCNDYRRAA	134	
Db	430	-----LFSWSPKVLGXQAXATTPSXXXF---V 453		
QY	135	VPGLFILFEL-----RHRCP-----TLTQDEVQWCDHSSLOPSTPEIKHPASA	178	
Db	454	FGGFFFFFALFLRXALALTPLRCSGKFWLTAASTSWV-QAILLLSPVXLGLQAWA	512	
QY	179	SQVAGT-----KDMHHYTWLIFIFNFRLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFSC	234	
Db	513	A-IPGXFWYFXRXHSFTMLI-----RLVSNXPQV-----ICPPG-----	546	
QY	235	PSLSSSWDYRR-PPRLANFFVFLVEMGFTMARLILISGPCDLPASASQSGAGITGVSHA	293	
Db	547	--LPKCDRREPPHPAPAXXLFL-----GVFFF-----	572	
QY	294	RLINFCLEFESHVSVTQAGVQW-----PNLGLSLQPLPPGLKRFSCLSLPSWMDYGLPHPP	350	
Db	573	--FFLLCFCFXRDLPLXHPG--WSNVAFGSLQPOPPGKRFSCLSLPCSWDYRAGPPFL	628	
QY	351	ANFCIFIRGGVSPYLSGWSQTPDLR 375		

```
Db      629 ANLCIFNRDVTSPCKSGMSQTPDLK 653

RESULT 2
C40201
artifact-warning sequence (translated ALU class C) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: C40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: C40201
A:Molecule type: DNA
A:Residues: 1-613 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match      15.5%; Score 315.5; DB 4; Length 613;
Best Local Similarity 33.4%; Pred. No. 5e-20;
Matches 98; Conservative 9; Mismatches 73; Indels 113; Gaps 8;

QY      6  LLPRLECNCAISAHNRNLRLPGSSDSPASASPVAGITGCTHARLILYFLVEMEFLLHVQ 65
DB      424  LSPRLCEGSAISAHCKLHLPLGCHSPASAFVCGTGTGARTMPS-XFFVFLVEMGFCHVQ 482
QY      66  AGLELPTSDPVSASQSARYRTGHHARLCLANFCGRNRVSLMCPSPKQSTCLSLP 125
DB      483  AGLELLAS-----XSTHLCILP 498
QY      126  KCWDYRR-----NAVGLFLFLFRLHRCPTLTODEVQWCHDSSLQSPTEIKHPPASA--- 178
DB      499  KCWDYRRLEPLHAPAXXFFFF-----XDRVSLC-----HPGWSAMAR 536
QY      179  SQVAGTKDMHHTWLIIFIFIFNFLRLSLNSVTQAGVQWRNLGSLQPLPPGFKLFSCPSLL 238
DB      537  SRLTASSRVRVAIL-----PQSAVYGLQAPA-- 565
QY      239  SSWDYRRPRLANFFVFLVEMGTFMFARILISGPCDLPASASQASAGITGVSH 291
DB      566  -----PCPANFLYFXKKWGFAMLARLVNSWPHDPTTFASQASAGITGVSH 610

RESULT 3
A40201
artifact-warning sequence (translated ALU class A) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: A40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: A40201
A:Molecule type: DNA
A:Residues: 1-627 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match      15.5%; Score 315.5; DB 4; Length 627;
```

```
Best Local Similarity 33.4%; Pred. No. 5.2e-20;
Matches 98; Conservative 13; Mismatches 67; Indels 115; Gaps 7;

QY      6  LLPRLECNCAISAHNRNLRLPGSSDSPASASPVAGITGCTHARLILYFLVEMEFLLHVQ 65
DB      436  LSPRLCEGSAISAHCKLHLPLGSRHSPASASQVAGTTGARTTPG-XFFVFLVETGHRGSQ 494
QY      66  AGLELPTSDPVSASQSARYRTGHHARLCLANFCGRNRVSLMCPSPKQSTCLSLP 125
DB      495  DGLDLTL-----XSASAR-----LGLP 510
QY      126  KCWDYRRAAVGLFLFLFRLHRCPTLTODEVQWCHDSSLQSPTEIKHPPASASQVAGTK 185
DB      511  KCWDYRRETAFG-----
QY      186  DMHHTWLIIFIFIF-----NFLRSLNSVTO-----AGVQWRNLGSLQPLPPGFKLFSCPS 236
DB      523  ---XXXFLFFVIFPRDGVSLCRQWSAVASRLTASSASRVHAILLPQPCKLGLQAPA 579
QY      237  LLSSWDYRRPRLANFFVFLVEMGTFMFARILISGPCDLPASASQASAGITGV 289
DB      580  L-----RPAFLYFXRRRGFTVVARMVVISXPRDPPALASQASAGITGV 622

RESULT 4
E40201
artifact-warning sequence (translated ALU class E) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: E40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: E40201
A:Molecule type: DNA
A:Residues: 1-597 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match      14.3%; Score 291.5; DB 4; Length 597;
Best Local Similarity 30.5%; Pred. No. 6.6e-18;
Matches 118; Conservative 24; Mismatches 106; Indels 139; Gaps 20;

QY      5  LLLPRLECNCAISAHNRNLRLPGSSD-SPASASPVAGITGCTHARLILYF-----FLVEM 58
DB      310  LLLPRPEYDGTISP--QTLPLPGKFQFSPVASASVAGITGMRHHAQLILYFXRWGFSMLV 367
QY      59  EFLHVQAGLELPTSDPVSASQSARYT-----GHHARLC 95
DB      368  KLVNSQPQVIRPALNSQSAGIT-GMSYHTWXXFFPFETFCSCCGRSTMAOSHRLK 426
QY      96  LANFCGRNRVSLMCPSPKQSTCLSLPCWDYRRAAVGLFLFLFRLHRCPTLTQDE 155
DB      427  ---FLGSSNLLSQP---PEX-----LGLQAC-----ATTPSXVIF-----SRDG 461
QY      156  V-----QWCHDSSLQSPTEIKHPPASASQVAGTKDMHHTWLIIFIFNFLRSLNSVT 210
DB      462  VSPCWSWSQTPNLRXSAPXT-PKALGLQAXATTP-----GXXXFFFLRRSFALVA 512
QY      211  QAGVQWRNLGSLQPLPPGF-----KLFCPSLLSSWDYRR--PRLANFVFLVEMGTFM 264
DB      513  QAGVRHNLTA-----NFAQSVQAILSCSLPSSDYRHAPPAPAN-FIFLVEGFL-- 563
QY      265  ARILISGFCDLPASASQSAGITGVSHHARLIFNFCFLFEMESHSVTQAGVQWPNLGLSQP 324
DB      564  -----HVGQAGLKLPTSGD--- 577
```

QY 325 LPPGLKRFSCLSLPSSWDYGHLPHPHA 351
Db 578 -PPRL- - - - -LPKWDYRHEPLHLA 597

RESULT 5
D40201
Artifact-warning sequence (translated ALU class D) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: D40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: D40201
A:Molecule type: DNA
A:Residues: 1-579 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potentially
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 9.7%; Score 197.5; DB 4; Length 579;
Best Local Similarity 28.1%; Pred. No. 1.4e-09;
Matches 81; Conservative 11; Mismatches 69; Indels 127; Gaps 10;

QY 12 CN-GAISHRNLRPGSSDSPASAPVAGITGCTHARLILYFLVEMEFHVGQAGLEL 70
Db 404 CNHGSLS- - - - -LDPPGQVILLPPQPEXGLQAYATRSXGLYLFVFEVGRHVAQAVLEL 459

QY 71 PTSDPPSVSASQSAARYTGHARLCLANFCGRNRSVLMCPMSWPELKQSTCLSLPKCWDY 130
Db 460 - - - - -LSWSIHLPW- - - - -LKKWDY 475

QY 131 RRAAV- - - - -PGFILFRLHRCPTLQDEVQWCHSSLOFSPTPEIKHPASASQVAG 183
Db 476 RRAAMLGXXKFRQGLMLPRLEYRGAIMA- - - - -HXAL- - - - -TSQV- - - 512

QY 184 TKDHHYTWLIFIFENFLRQSLNSVTQAGVQWRNLGSLQPLPPGFKLPCSPSLSSWDY 243
Db 513 - - - - -KXSSCPSLSSWDY 526

QY 244 R-RPPRLANFFV-FLVEMGFTMFARLILSGPCDLPASASQAGITGV 289
Db 527 RLMLPDLANFCIFFLXRWGFDMPLRLFLNSXAGAYTCHGSXAGITGV 574

RESULT 6
S65657
alpha-1C-adrenergic receptor splice form 2 - human
N:Alternate names: alpha-1C-adrenoceptor isoform 2
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S65657; S65655
R:Tanaka, T.
submitted to the EMBL Data Library, July 1994
A:Reference number: S65656
A:Accession: S65657
A:Molecule type: mRNA
A:Residues: 1-499 <TAN>
A:Cross-references: UNIPROT:Q13675; EMBL:D32202; NID:G927208; PIDN:BAA06901.1; PID:G9272
R:Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1995
A:Title: Cloning, functional expression and tissue distribution of human alpha (1C)-adren
A:Reference number: S65654; MUID:95255557; PMID:7737411
A:Accession: S65655
A:Molecule type: mRNA

A:Residues: 424-499 <HIR>
A:Cross-references: EMBL:D32202
C:Genetics:
A:Gene: GDB:ADRA1C; ADRA1L1
A:Cross-references: GDB:I28088; OMIM:104221
A:Map position: 8p21-8p11.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 8.6%; Score 175; DB 2; Length 499;
Best Local Similarity 58.0%; Pred. No. 1.1e-07;
Matches 40; Conservative 5; Mismatches 20; Indels 4; Gaps 1;

QY 9 RLECNCAISAHNLRPGSSDSPASAPVAGITGMC- - - - -THARLILYFLVEMEFHVG 64
Db 431 RLECSGMILAHCNLRPGSRDSPASASQAAGTGDVPGRRHQAQLIFVLVETGFHHVG 490

QY 65 QAGLELPTS 73
Db 491 QDDLDLLTS 499

RESULT 7
I54375
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Aug-2004
C:Accession: I54375
R:Arakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
Hum. Mol. Genet. 3, 565-568, 1994
A:Title: Alternative splicing of the NF2 gene and its mutation analysis of breast and c
A:Reference number: I54375; MUID:94348501; PMID:8069299
A:Accession: I54375
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-46 <RES>
A:Cross-references: UNIPROT:Q16230; GB:S73853; NID:G688372; PIDN:AAB31736.1; PID:G68837
C:Genetics:
A:Gene: GDB:NF2
A:Cross-references: GDB:I20232; OMIM:101000
A:Map position: 22q12.2-22q12.2
C:Superfamily: laminin-type EGF-like homology

Query Match 8.2%; Score 167; DB 2; Length 46;
Best Local Similarity 76.2%; Pred. No. 3.6e-08;
Matches 32; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 302 FEMESHVTOAGVQVQWPNLGLSLQPLPPGLKRFSCLSLPSSWDY 343
Db 4 FNCESCSVTLAGVQWRDLGLLQPLPPKRFKRFSCLSFPSSWDY 45

RESULT 8
I78885
serine/threonine-specific protein kinase (EC 2.7.1.1-) STK2 - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I78885
R:Lievadaku, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simm
Oncogene 9, 1977-1988, 1994
A:Title: Two novel human serine/threonine kinases with homologies to the cell cycle reg
A:Reference number: I58396; MUID:94268838; PMID:8208544
A:Accession: I78885
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-841 <RES>
A:Cross-references: UNIPROT:P51957; GB:L20321; NID:G348244; PIDN:AAA36658.1; PID:G34824
C:Genetics:
A:Gene: GDB:STK2
A:Cross-references: GDB:374125
A:Map position: 3p21.1-3p21.1
C:Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol
C:Keywords: phosphotransferase

F;4-261/Domain: protein kinase homology <KIN>

Query Match 7.9%; Score 161; DB 1; Length 841;
Best Local Similarity 46.2%; Pred. No. 3.6e-06;
Matches 42; Conservative 14; Mismatches 25; Indels 10; Gaps 4;

QY 6 LLPRLECNCAISAHRNLRLPFGSSDSPASASPVAGITGMCTHAR-LILYFFLVEMEFHVHG 64
DB 460 LSPKLECSGTIIAHSNLRLLGSSDSPASASRVAGITGVCHHAQQVAGECIIEKQ-----G 515

QY 65 QAGLELP---TSDDPSVSAS--QSARYRTGH 90
DB 516 RIHPDLQPHNSGSEPSLSRQRKREQTEH 546

RESULT 9
I54374
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I54374
R:Pykett, M.J.; Murphy, M.; Harnish, P.R.; George, D.L.
Hum. Mol. Genet. 3, 559-564, 1994
A:Title: The neurofibromatosis 2 (NF2) tumor suppressor gene encodes multiple alternative
A:Reference number: I54374; MUID:94348500; PMID:8069298
A:Accession: I54374
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-39 <RES>
A:Cross-references: UNIPROT:Q16230; GB:I27065; NID:G463120; PIDN:AAA62422.1; PID:G463121
C:Genetics:
A:Gene: GDB:NF2
A:Cross-references: GDB:120232; OMIM:101000
A:Map position: 22q12.2-22q12.2
C:Superfamily: laminin-type EGF-like homology

Query Match 7.7%; Score 157; DB 2; Length 39;
Best Local Similarity 78.9%; Pred. No. 2.3e-07;
Matches 30; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 306 SHSVTQAGVQWPNLGSLOPLPGLKRFSCLSLPSWDY 343
DB 1 SCSVTLAGVQWRDLGLQLPLPKPKFKFSCLSLPSWDY 38

RESULT 10
B40201
artifact-warning sequence (translated ALU class B) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C:Accession: B40201
R:Claverie, J.M.
personal communication, 1992
A:Reference number: A40201
A:Accession: B40201
A:Molecule type: DNA
A:Residues: 1-301 <CLA>
R:Claverie, J.M.
Genomics 12, 838-841, 1992
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential
A:Reference number: A40200; MUID:92241891; PMID:1572661
A:Contents: annotation
C:Comment: this "warning" entry is a conceptual translation in all 6 reading frames of c
in-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 7.4%; Score 151.5; DB 4; Length 301;
Best Local Similarity 22.4%; Pred. No. 7.6e-06;
Matches 66; Conservative 15; Mismatches 45; Indels 169; Gaps 10;

QY 6 LLPRLECNCAISAHRNLRLPFGSSDSPASASPVAGITGMCT-----HARILLYFFLVEMEF 60

DB 158 MLPKLVNWSQAIIILQHP-----KVLGLQMLATMPCXXXTQLILFPF----- 211

QY 61 LHVGQAGLELPTSDPSVSASQSARYRTGHHARCLANFCGRNRYSLMCPSPWS--PELKQ 118
DB 212 -----YRAG-----VLLCCPSWSXTPGLKQ 231

QY 119 STCLSLPKCWYRRAAVPGLFLFLFRLHRCPTLTQDEVQWQDHSSLSQSTPIKHPASA 178
DB 232 SSYFSPKCDWYR-----C-----XFFCPA 251

QY 179 SOVAGTKDMHYTWLIFIFNFLQSLNSVTAQVQWRNLGSLQLPFGFKLFSCLPSLL 238
DB 252 XXXPSX-----FYFIFELGSCYVAQALE----- 276

QY 239 SSWDYRRPRLANFFVFLVEMGFTWFARLIILISGCDLPASASQAGITGVSHHA 293
DB 277 -----LLVSSNP---PTSASQAGITDVSHHA 300

RESULT 11
A46010
X-linked retinopathy protein (C-terminal, clone XEH.8c) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46010
R:Wong, P.; Macdonald, I.M.; Sood, R.; Smith, C.; Pilon, R.; Tenniswood, M.
Genomics 15, 467-471, 1993
A:Title: Identification and partial characterization of a candidate gene for X-linked re
A:Reference number: A46010; MUID:93224131; PMID:8468040
A:Accession: A46010
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-100 <WON>
A:Cross-references: UNIPROT:Q07826; GB:S58722; NID:G299470; PIDN:AAB26149.1; PID:G299471
A>Note: sequence extracted from NCBI backbone (NCBIN:129339, NCBI:129340)

Query Match 6.9%; Score 139.5; DB 2; Length 100;
Best Local Similarity 34.2%; Pred. No. 2.5e-05;
Matches 38; Conservative 6; Mismatches 22; Indels 45; Gaps 2;

QY 197 FIFNFLQSLNSVTAQVQWRNLGSLQLPFGFKLFSCLPSLSSWDYRRPRLANFFVFL 256
DB 1 FFFPFETESCVAEAGVQWCDLGLSKSPPP----- 31

QY 257 VEMGFTMPARLILISGCDLPASASQAGITGVSHARLIINFCLFEMESH 307
DB 32 -----GSSDSPASASRVAGITGMHHHTQLIFVP-LVETGSH 66

RESULT 12
A56194
thromboxane A-2 receptor, endothelial - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56194
R:Raychowdhury, M.K.; Yukawa, M.; Collins, L.J.; McGrail, S.H.; Kent, K.C.; Ware, J.A.
J. Biol. Chem. 270, 7011, 1995
A:Reference number: A56194; MUID:95204505; PMID:7896853
A:Accession: A56194
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-79 <RAY>
A:Cross-references: UNIPROT:Q9UCY2; GB:U11271
C:Superfamily: prostaglandin E receptor EPI

Query Match 6.8%; Score 137.5; DB 2; Length 79;
Best Local Similarity 49.3%; Pred. No. 2.8e-05;
Matches 37; Conservative 8; Mismatches 25; Indels 5; Gaps 2;

QY 6 LLPRLECNCAISAHRNLRLPFGSSDSPASASPVAGITGMCTHARLILYFFLVEMEFHVHG 65
DB 5 LWPSEYSGTISAHNCLNLRPLGSSDSRASASRAAGITGV-SHCARPCMLFDPEFDLL---- 59


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Db 152 -----STAVECKKSC-PNPGEIRN---CQIDVPG-----G 179
QY 193 LIFIFINF-----LRQSLNS---VTQAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWD 242
Db 180 ILFGATISFSCNTGKLFQSTSSFCILIGSSVQWSD-----ELPECREIY-CPA----- 227
QY 243 YRRPRLANFFV-----FLVEMGFTWPARLILI-----SGP----- 273
Db 228 ---PQIDNGIIOGERDHYGRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECR 284
QY 274 -----CDLP-----ASASOSAGITGVSHH----- 292
Db 285 GKSLTSKVPTVQKPTTVNVPTEVSPISQTKTTTTPNAQATRSTPVSRTHKHETH 344
QY 293 -----ARLIFNCLFEMESHVTVQAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWD 341
Db 345 PNKGSOTTSCTTRLISG-----SRPVTQAGMRWCDRSSLSQSRTPGFKRSFHFSLPSSW 397
QY 342 DY 343
Db 398 YY 399
```

Search completed: September 13, 2005, 19:35:16
Job time : 21 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2034	100.0	375	3	AA801399	Neuron-as
2	2034	100.0	375	5	AB881538	Neural th
3	2034	100.0	375	5	AA829142	AD7C-NTP
4	2034	100.0	375	6	ABR63268	AD7C-NTP
5	2034	100.0	375	6	ADA84017	Human POM
6	2034	100.0	375	6	ABU03024	Human neu
7	2034	100.0	375	6	AB899774	Amino aci
8	2034	100.0	375	6	ABU19445	AD7C-neur
9	2034	100.0	375	7	ABR37642	Human neu
10	2034	100.0	375	8	ADR14409	Human NP-
11	1415.5	69.6	397	2	AA895913	Neural th
12	928	45.6	381	4	AAU30235	Novel hum
13	927.5	45.6	382	4	AAU32610	Novel hum
14	927.5	45.6	382	4	AAU31818	Novel hum
15	927.5	45.6	382	4	AAU32707	Novel hum
16	849	41.7	324	4	AAU29573	Novel hum
17	849	41.7	324	4	AAU29579	Novel hum
18	822.5	40.4	411	4	ABG08428	Novel hum
19	739	36.3	317	4	AAU33200	Novel hum
20	735	36.1	290	4	ABG21913	Novel hum
21	734.5	36.1	361	5	ABG68738	Human pro
22	729	35.8	449	5	ABU01057	Human pro
23	701.5	34.5	332	5	ADK34410	Ovary cel
24	609	29.9	257	4	AAO10294	Novel hum
25	590	29.0	276	4	ABG07919	Human pol

PS	Disclosure; Page 143-144; 145pp; English.	DE	Neural thread protein (NTP).
XX		XX	
CC	Human neuron-associated proteins (NEUP) can be used for treating or	KW	Neural thread protein; NTP; Harilil peptide; Alzheimer's disease;
CC	preventing a disorder associated with decreased expression or activity of	KW	Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
CC	NEUP. Antagonists of NEUP are useful for treating or preventing	XX	hypoxia; ischaemia; cerebral infarction.
CC	disorder associated with increased expression or activity of NEUP. NEUP	OS	Homo sapiens.
CC	or their fragments or derivatives are useful for treating neurological	XX	
CC	disorder such as epilepsy, ischemic cerebrovascular disease, stroke,	XX	WO200234915-A2.
CC	cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's	PN	
CC	disease, dementia and Parkinson's disease. NEUPs are also useful for	XX	
CC	treating other demyelinating diseases, bacterial and viral meningitis,	PD	02-MAY-2002.
CC	prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and	XX	
CC	metabolic diseases of the nervous system, neurofibromatosis, other	PF	25-OCT-2001; 2001WO-US042813.
CC	developmental disorders of the central nervous system, cerebral palsy,	XX	
CC	neurolept disorders, autonomic nervous system disorders, cranial	XX	
CC	nerve disorders, spinal cord diseases, muscular dystrophy and other	PR	27-OCT-2000; 2000US-00697590.
CC	neuromuscular disorders, peripheral nervous system disorders, inherited,	PA	(NYMO-) NYMOX PHARM CORP.
CC	metabolic, endocrine, and toxic myopathies, mental disorders including,	XX	
CC	mood, anxiety and schizophrenic disorders, a cell proliferative disorder	PI	Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
CC	such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,	XX	
CC	cirrhosis, hepatitis, mixed connective tissue disease (MCTD),	XX	
CC	myelofibrosis, paroxysmal nocturnal haemoglobinuria, cancers of the	DR	WPI; 2002-507998/54.
CC	adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an	XX	N-PSDB; ABN89470.
CC	autoimmune/inflammatory disorder such as acquired immunodeficiency	PT	New Harilil peptide sequences of the Neural Thread protein, useful in
CC	sndrome (AIDS), Addison's disease, adult respiratory distress syndrome,	CC	therapeutic assays, e.g. as targets for developing drugs for treating
CC	allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, Werner	PT	Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
CC	syndrome, complications of cancer, hemodialysis, and extracorporeal	PT	these diseases.
CC	circulation, viral, bacterial, fungal parasitic, protozoal, and	XX	
CC	helminthic infections, and trauma. This protein was designated g3002527	XX	
XX		PS	Example 1; Fig 1; 53pp; English.
SQ	Sequence 375 AA;	XX	
Query Match	100.0%; Score 2034; DB 3; Length 375;	CC	The present invention describes a neural thread protein (NTP) peptide
Best Local Similarity	100.0%; Pred. No. 1e-198;	CC	having an amino acid sequence selected from ABB81511 to ABB81529 and
Matches 375; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	CC	their homologues, which are referred collectively as Harilil peptides (1).
		CC	(1) have neuroprotective, nootropic, vasotropic and cerebroprotective
		CC	activities, and can be used in peptide therapy. The Harilil peptide
		CC	sequences can be used as analogues for NTP in therapeutic or diagnostic
		CC	assays by replacing NTP with the peptide in such an assay. The Harilil
		CC	peptides are also useful as a trap material in a diagnostic or
		CC	therapeutic assay. Therefore, the Harilil peptides are useful in binding
		CC	assays, protein and antibody purification, therapeutics or diagnostics.
		CC	In particular, the peptides are also useful for diagnosing Alzheimer's
		CC	disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
		CC	glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
		CC	are also useful as targets for drug development for the treatment of
		CC	these diseases. The present sequence represents a neural thread protein
		CC	given in the exemplification of the present invention
		XX	
		SQ	Sequence 375 AA;
Query Match	100.0%; Score 2034; DB 5; Length 375;	QY	1 MEPSLLLPRLCNGAISAHNRLLPGSSDPSASPVAGITGCTHARILILYFFLVEMEF 60
Best Local Similarity	100.0%; Pred. No. 1e-198;	Db	1 MEPSLLLPRLCNGAISAHNRLLPGSSDPSASPVAGITGCTHARILILYFFLVEMEF 60
Matches 375; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
		QY	61 LHVGAGLELPTSDPSVSASQARYRTGHHARILCLANFCGRRVSLMCPSPSPKQST 120
		Db	61 LHVGAGLELPTSDPSVSASQARYRTGHHARILCLANFCGRRVSLMCPSPSPKQST 120
		QY	121 CLSLPKCWDYRAAIVPGLFILFHLRCPPTLTQDEVQWCHSSLOPSPTEIKHPASASQ 180
		Db	121 CLSLPKCWDYRAAIVPGLFILFHLRCPPTLTQDEVQWCHSSLOPSPTEIKHPASASQ 180
		QY	181 VAGTKDMHHYTWLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLLSS 240
		Db	181 VAGTKDMHHYTWLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLLSS 240
		QY	241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARILIFNFC 300
		Db	241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARILIFNFC 300
		QY	301 LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
		Db	301 LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
		QY	361 VSPYLSGWSQTPDLR 375
		Db	361 VSPYLSGWSQTPDLR 375
RESULT 2			
ABB81538			
ID	ABB81538 standard; protein; 375 AA.		
XX			
AC	ABB81538;		
XX			
DT	02-SEP-2002 (first entry)		
XX			

QY 301 LFMESHVSTQAGVQWPNLGSQPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
 DB |||||
 QY 301 LFMESHVSTQAGVQWPNLGSQPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
 DB |||||
 QY 361 VSPYLSGWSQTPDLR 375
 DB |||||
 QY 361 VSPYLSGWSQTPDLR 375
 DB |||||

RESULT 3

AAE29142

ID AAE29142 standard; protein; 375 AA.

XX

AC AAE29142;

XX

DT 27-JAN-2003 (first entry)

XX

DE AD7c-NTP protein.

XX

KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
 KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
 KW inflammatory disease; nutritional deficiency disease; genetic disease;
 KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
 KW infectious disease; congenital malformation; enzyme deficiency disease;
 KW amyloid disease; fibrosis disease; storage disease; radiation disease;
 KW poisoning; environmental disease; endocrine disease; protein therapy;
 KW degenerative disease; mechanical disease; AD7c-NTP protein.

OS Unidentified.

XX

XX WO200274323-A2.

PN

PD 26-SEP-2002.

XX

XX 08-MAR-2002; 2002WO-1B001959.

XX

XX 08-MAR-2001; 2001US-0273957P.

PR

PA (AVER/) AVERBACK P.

XX

XX Averbach P;

XX

XX WPI; 2002-759864/82.

DR

DR N-PSDB; AAD46671.

XX

PT Treating a condition in a patient requiring removal or destruction of
 PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
 PT disease, comprises administering a neural thread protein (NTP) or a NTP
 PT gene to a mammal.

PS

XX Example 2; Fig 1; 70pp; English.

XX

CC The invention relates to a method for treating a condition in a patient
 CC requiring removal or destruction of cells. The method involves
 CC administering to a mammal a neural thread protein (NTP), or administering
 CC to a tumour or other target cell a NTP gene, where the expression of the
 CC NTP gene is induced resulting in expression of the NTP protein. The
 CC method and NTP are useful for treating a condition in a patient requiring
 CC removal or destruction of cells, such as a benign or malignant tumour of
 CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
 CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
 CC bacterially, or parasitically altered tissue, or a malformation of a
 CC tissue. Other conditions include a cosmetic modification to a tissue,
 CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
 CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
 CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
 CC disease, metabolic disease, hereditary/genetic disease, traumatic disease,
 CC or physical injury, nutritional deficiency disease, infectious disease,
 CC congenital malformation, amyloid disease, fibrosis disease, storage
 CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
 CC disease, radiation disease, environmental disease, endocrine disease or
 CC mechanical disease. The invention is useful in protein therapy and gene
 CC therapy. The present sequence is AD7c-NTP protein

XX Sequence 375 AA;
 SQ
 Query Match 100.0%; Score 2034; DB 5; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-198;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEFSLLLPRLECNCAISAHNRNLRLPGSSDSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 DB |||||
 QY 1 MEFSLLLPRLECNCAISAHNRNLRLPGSSDSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 DB |||||
 QY 61 LHVGQAGLELPTSDSPVSASOSARYRTGTHARLCLANFCGNNRVSLMCPSPSPKQST 120
 DB |||||
 QY 61 LHVGQAGLELPTSDSPVSASOSARYRTGTHARLCLANFCGNNRVSLMCPSPSPKQST 120
 DB |||||
 QY 121 CLSLPKCWDYRAAVPGLPILFFLHRRCPTLTQDSVQWCDHSSLOPSTPEIKHPASASQ 180
 DB |||||
 QY 121 CLSLPKCWDYRAAVPGLPILFFLHRRCPTLTQDSVQWCDHSSLOPSTPEIKHPASASQ 180
 DB |||||
 QY 181 VAGTKDMEHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLGSIQLPPGKLFSCPSLLSS 240
 DB |||||
 QY 181 VAGTKDMEHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLGSIQLPPGKLFSCPSLLSS 240
 DB |||||
 QY 241 WDYRPPRLANFFVFLVEMGTMTFARLILISGPCDLPASASQAGITGVSHARLIFNFC 300
 DB |||||
 QY 241 WDYRPPRLANFFVFLVEMGTMTFARLILISGPCDLPASASQAGITGVSHARLIFNFC 300
 DB |||||
 QY 301 LFMESHVSTQAGVQWPNLGSQPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
 DB |||||
 QY 301 LFMESHVSTQAGVQWPNLGSQPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
 DB |||||
 QY 361 VSPYLSGWSQTPDLR 375
 DB |||||
 QY 361 VSPYLSGWSQTPDLR 375
 DB |||||

RESULT 4

ABR63268

ID ABR63268 standard; protein; 375 AA.

XX

AC ABR63268;

XX

DT 28-AUG-2003 (first entry)

XX

DE AD7c-NTP protein.

XX

KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;

KW neural thread protein; NTP; tumour.

XX

OS Unidentified.

XX

PN WO2003008443-A2.

XX

PD 30-JAN-2003.

XX

PF 19-JUL-2002; 2002WO-CA001105.

XX

PR 19-JUL-2001; 2001US-0306150P.

XX

PR 19-JUL-2001; 2001US-0306161P.

XX

PR 16-NOV-2001; 2001US-0331477P.

XX

PA (NYMO-) NYMOX CORP.

XX

PI Averbach PA;

XX

XX WPI; 2003-247999/24.

XX

PT Novel neural thread protein peptide, referred as cell death peptide,
 PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
 PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 1; 77pp; English.

PS

XX

CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 2034; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-198;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
DB 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
QY 61 LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRVSLMCPSPKELKOST 120
DB 61 LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRVSLMCPSPKELKOST 120
QY 121 CLSLPKCWDYRAAVPGLFILFELRHRCPTLTQDEVQWCHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCWDYRAAVPGLFILFELRHRCPTLTQDEVQWCHSSLOPSTPEIKHPPASASQ 180
QY 181 VAGTKDMHHYTWLIFIFNFRLOSNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLSS 240
DB 181 VAGTKDMHHYTWLIFIFNFRLOSNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLSS 240
QY 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
QY 301 LFEMESHVTOAGVQWPNLGSLOPLPPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVTOAGVQWPNLGSLOPLPPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 5
ID ADA84017 standard; protein; 375 AA.
XX ADA84017;
XX 20-NOV-2003 (first entry)
XX Human POM80 protein.
XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX Homo sapiens.
XX WO2002103028-A2.
XX 27-DEC-2002.
XX 30-MAY-2002; 2002WO-1B004189.
XX 30-MAY-2001; 2001US-0293999P.
PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.
XX (BIOM-) BIOMEDICAL CENT.
PA Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
DR N-PSDB; ADA84016.
XX Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 29; Page 398-400; 516pp; English.
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 2034; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-198;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
DB 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
QY 61 LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRVSLMCPSPKELKOST 120
DB 61 LHVQAGLELPTSDPSVSASQSAARYRTGTHARLCLANFCGRNRVSLMCPSPKELKOST 120
QY 121 CLSLPKCWDYRAAVPGLFILFELRHRCPTLTQDEVQWCHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCWDYRAAVPGLFILFELRHRCPTLTQDEVQWCHSSLOPSTPEIKHPPASASQ 180
QY 181 VAGTKDMHHYTWLIFIFNFRLOSNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLSS 240
DB 181 VAGTKDMHHYTWLIFIFNFRLOSNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLSS 240
QY 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
QY 301 LFEMESHVTOAGVQWPNLGSLOPLPPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVTOAGVQWPNLGSLOPLPPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 6
ABU03024

ID XX
AC XX
XX XX
DT XX
XX XX
DE XX
XX XX
KW ABO03024 standard; protein; 375 AA.
AC ABO03024;
XX XX
DT 20-JAN-2003 (first entry)
XX XX
DE Human neural thread protein AD7C-NTP.
XX XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumor; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX XX
OS Homo sapiens.
XX XX
FN WO200297030-A2.
XX XX
PD 05-DEC-2002.
XX XX
PP 24-MAY-2002; 2002WO-CA000759.
XX XX
PP 25-MAY-2001; 2001US-0293156P.
XX XX
PA (NYMO-) NYMOX CORP.
XX XX
PI Averbach PA;
XX XX
DR WPI; 2003-041406/03.
XX XX
PT Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX XX
PS Disclosure; Fig 1; 78pp; English.
XX XX
CC The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This is the amino acid sequence of the human neural thread
XX XX
protein AD7C-NTP

SQ Sequence 375 AA;
Query Match 100.0%; Score 2034; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-198;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASAPVAGITGCTHARLILYFFLYEMERF 60
DB 1 MEFSLLPRLCNGAISAHNRNLRPGSSDSPASAPVAGITGCTHARLILYFFLYEMERF 60
QY 61 LHVGQAGLELPTSDPSVSASQASARYTGHARLCLANPCGNRVSLMCPSPKQST 120
DB 61 LHVGQAGLELPTSDPSVSASQASARYTGHARLCLANPCGNRVSLMCPSPKQST 120
QY 121 CUSLPCXNDYRAAAYVGLFLLFRLHRCPTLTQDEVQWCDHSSLOPSTEIKHPPASQ 180
DB 121 CUSLPCXNDYRAAAYVGLFLLFRLHRCPTLTQDEVQWCDHSSLOPSTEIKHPPASQ 180
QY 181 VAGTKDMHHYTWLIFIFNFRLQSLNSVTQAGVQWNLGSLQPLPPGFKLFCSPCLLS 240
DB 181 VAGTKDMHHYTWLIFIFNFRLQSLNSVTQAGVQWNLGSLQPLPPGFKLFCSPCLLS 240
QY 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHARLIFNFC 300
DB 241 WDYRPPRLANFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHARLIFNFC 300
QY 301 LFEMESHVSTQAGVQWNLGSLQPLPPGFKLFCSPCLLSQPLPPGFKLFCSPCLLS 360
DB 301 LFEMESHVSTQAGVQWNLGSLQPLPPGFKLFCSPCLLSQPLPPGFKLFCSPCLLS 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375
RESULT 7
ABB99774
ID ABB99774 standard; protein; 375 AA.
AC ABB99774;
XX XX
DT 24-MAR-2003 (first entry)
XX XX
DE Amino acid sequence of human neuronal thread protein AD7C-NTP.
XX XX
KW Human; neuronal thread protein; AD7C-NTP; Alzheimer's disease; histone;
KW neurodegeneration; in vivo gene expression; amphipathic compound;
XX XX
OS Homo sapiens.
XX XX
FN WO200299036-A2.
XX XX
PD 12-DEC-2002.
XX XX
PP 28-MAY-2002; 2002WO-US016429.
XX XX
PR 01-JUN-2001; 2001US-00872968.
XX XX
PA (RHOD-) RHODE ISLAND HOSPITAL.
XX XX
PI Wands JR, De La Monte SM;
XX XX
DR WPI; 2003-140605/13.
DR N-PSDB; ABZ23236.
XX XX
PT Inducing prolonged in vivo gene expression in mammal by contacting
PT neuronal tissue with composition comprising Alzheimer's disease-
PT associated neural thread protein 7c antisense nucleic acid, histone,
PT amphipathic compound.
XX XX
PS Disclosure; Page 35; 69pp; English.
XX XX

CC The present sequence represents a human neuronal thread protein AD7c-NTP.
 CC AD7c-NTP is overexpressed in brains with Alzheimer's disease at early and
 CC intermediate stages of neurodegeneration. The expression of AD7c-NTP may
 CC be reduced using the method of the invention. The specification describes
 CC a method for inducing prolonged in vivo gene expression in a mammal. The
 CC method comprises contacting a non-muscular tissue with a composition
 CC comprising a nucleic acid, histone and an amphipathic compound. The
 CC method is useful for inducing prolonged in vivo gene expression in non-
 CC muscular tissue of a mammal, e.g. neuronal tissue, central nervous system
 CC (CNS) tissue, tissue comprising a post-mitotic neuronal cell, cortical
 CC neuronal cell or hippocampal neuronal cell, glial cell, or vascular
 CC endothelial cell. The method is useful in gene therapy applications to
 CC treat Alzheimer's disease, where the composition comprises antisense
 CC AD7c-NTP nucleic acid

SQ Sequence 375 AA;

Query Match 100.0%; Score 2034; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-198;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPRLECNCAISAHNRNLRPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLLPRLECNCAISAHNRNLRPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60

QY 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPKELKOST 120
 DB 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPKELKOST 120

QY 121 CLSLPKCDWYRAAIVPGLFIFLFRHRCPTLTQDEVQWCHDSSLOPSTPEIKHPPASASQ 180
 DB 121 CLSLPKCDWYRAAIVPGLFIFLFRHRCPTLTQDEVQWCHDSSLOPSTPEIKHPPASASQ 180

QY 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
 DB 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240

QY 241 WDYRRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 DB 241 WDYRRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300

QY 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360
 DB 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360

QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375

RESULT 8

ABU19445
 ID ABU19445 standard; protein; 375 AA.
 XX
 AC ABU19445;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE AD7C-neural thread protein.
 XX
 KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN WO200292115-A2.
 XX
 PD 21-NOV-2002.
 XX
 PP 16-MAY-2002; 2002WO-CA000712.
 XX
 PR 16-MAY-2001; 2001US-0290971P.
 XX

PA (NYMO-) NYMOX CORP.
 XX
 FI Averbach PA;
 XX
 DR WPI; 2003-129234/12.
 DR N-PSDB; AAL54224.
 XX
 PT Preventing and/or inhibiting cell death and/or tissue necrosis in a
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's
 PT disease, by contacting the live tissue with at least one segment of
 PT neural thread proteins (NTP).
 XX
 PS Disclosure; Fig 1; 60pp; English.
 XX
 CC The invention relates to a novel method for preventing and/or inhibiting
 CC cell death and/or tissue necrosis in a tissue comprising contacting the
 CC live tissue with at least one segment of neural thread proteins (NTP).
 CC The methods are composition are useful for treating a neurodegenerative
 CC disorder, such as Alzheimer's disease. This sequence represents the AD7C-
 CC NTP protein relating to the invention
 XX

SQ Sequence 375 AA;

Query Match 100.0%; Score 2034; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-198;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPRLECNCAISAHNRNLRPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLLPRLECNCAISAHNRNLRPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60

QY 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPKELKOST 120
 DB 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPKELKOST 120

QY 121 CLSLPKCDWYRAAIVPGLFIFLFRHRCPTLTQDEVQWCHDSSLOPSTPEIKHPPASASQ 180
 DB 121 CLSLPKCDWYRAAIVPGLFIFLFRHRCPTLTQDEVQWCHDSSLOPSTPEIKHPPASASQ 180

QY 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
 DB 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240

QY 241 WDYRRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 DB 241 WDYRRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300

QY 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360
 DB 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360

QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375

RESULT 9

ADB37642
 ID ADB37642 standard; protein; 375 AA.
 XX
 AC ADB37642;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human neural thread protein AD7c-NTP.
 XX
 KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7C-NTP;
 XX
 OS Homo sapiens.
 XX

PN WO2003008444-A2.
 XX 30-JAN-2003.
 XX 19-JUL-2002; 2002WO-CA001106.
 XX 19-JUL-2001; 2001US-0306150P.
 PR 19-JUL-2001; 2001US-0306150P.
 PR 16-NOV-2001; 2001US-0331477P.
 XX (NYMO-) NYMOX CORP.
 XX
 XX Averbach PA, Gemmell J;
 DR WPI; 2003-248000/24.
 DR N-PSDB; ADB37519.
 XX
 PT Novel Related peptide or AD7c-neural thread peptide, useful for treating
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial
 PT hair, warts and unwanted fatty tissue.
 XX
 PS Disclosure; Fig 1; 109pp; English.
 XX
 CC The present invention relates to AD7c-neural thread protein (NTP) and
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are
 CC useful for treating a condition in a patient requiring removal or
 CC destruction of cells. The condition can be selected from benign or
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a
 CC tissue, virally, bacterially or parasitically altered tissue, or
 CC malformation of a tissue, where the tissue is selected from lung, breast,
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary
 CC gland, blood, brain and its coverings, spinal cord and its coverings,
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,
 CC hereditary/genetic disease, traumatic disease or physical injury,
 CC nutritional deficiency disease, infectious disease, amyloid disease,
 CC fibrosis disease, storage disease, congenital malformation, enzyme
 CC deficiency disease, poisoning, intoxication, environmental disease,
 CC radiation disease, endocrine disease, degenerative disease and mechanical
 CC disease. The peptides are useful for treating unwanted cellular
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that
 CC recognize and/or bind to Related proteins, Related peptides or NTP
 CC peptides. The present sequence is AD7c-NTP, used to illustrate the
 CC invention. AD7c-NTP is a ~41kd membrane associated phosphoprotein with
 CC functions associated with neuritic sprouting.
 XX
 SQ Sequence 375 AA;
 Query Match 100.0%; Score 2034; DB 7; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-198;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEFSLLLPLECNGAISAHNRLRLPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLLPLECNGAISAHNRLRLPGSSDPSASPVAGITGCTHARLILYFFLVEMEF 60
 QY 61 LVHQAGLELPTSDPSVASQASARYTGHARLCLANFCGRNRYSLMCPSPSELKQST 120
 DB 61 LVHQAGLELPTSDPSVASQASARYTGHARLCLANFCGRNRYSLMCPSPSELKQST 120
 QY 121 CLSLPKCWDYRAAVPGLFPLFLRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 DB 121 CLSLPKCWDYRAAVPGLFPLFLRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 QY 181 VAGTKDMHHYTWLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPGPKLFCSPCLSS 240

DB 181 VAGTKDMHHYTWLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPGPKLFCSPCLSS 240
 QY 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHARLIFNFC 300
 DB 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHARLIFNFC 300
 QY 301 LFEMESHSVTQAGVQWRNLGSLQPLPGPKLFCSPCLSSWDYGHLPHPANFCIFIRGG 360
 DB 301 LFEMESHSVTQAGVQWRNLGSLQPLPGPKLFCSPCLSSWDYGHLPHPANFCIFIRGG 360
 QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375
 RESULT 10
 ADR14409
 ID ADR14409 standard; protein; 375 AA.
 XX
 AC ADR14409;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human NF-kappaB pathway-associated protein SeqID410.
 KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnary; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HIV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.
 OS Homo sapiens.
 XX WO2004065577-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 13-JAN-2004; 2004WO-US0000798.
 XX
 PR 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-046957P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Nadler SG, Neubauer MG, Feder JN, Carman J;
 XX
 DR WPI; 2004-562169/54.
 XX N-PSDB; ADR14408.
 PT New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX
 PS Claim 6; SEQ ID NO 410; 237pp; English.
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypergenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2034; DB 8; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-198;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEFSLLPLRLCNGAISAHRLNRLPGSSDSPASAPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLPLRLCNGAISAHRLNRLPGSSDSPASAPVAGITGCTHARLILYFFLVEMEF 60
 QY 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPWSPKQST 120
 DB 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPWSPKQST 120
 QY 121 CLSLPKCDYRAAAYVGLFELFELHRCPTLTQDEVQWCHSSLOBSPEIKHPPASASQ 180
 DB 121 CLSLPKCDYRAAAYVGLFELFELHRCPTLTQDEVQWCHSSLOBSPEIKHPPASASQ 180
 QY 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWNLGSLQPLPPGKLFSCPSLLSS 240
 DB 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWNLGSLQPLPPGKLFSCPSLLSS 240
 QY 241 WYRRPPRLANFVFLVEMGFTWFAFLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 DB 241 WYRRPPRLANFVFLVEMGFTWFAFLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 QY 301 LFEMESHVSTQAGVQWNLGSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
 DB 301 LFEMESHVSTQAGVQWNLGSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
 QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375

RESULT 11
 ID AAR95913
 XX AAR95913 standard; protein; 397 AA.
 AC AAR95913;
 XX
 DT 13-NOV-1996 (first entry)
 DE Neural thread protein.
 DE
 KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
 KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
 XX binding fragment.
 XX
 OS Homo sapiens.

XX WO9615272-A1.
 PN 23-MAY-1996.
 PD 14-NOV-1995; 95WO-US017111.
 PF 14-NOV-1994; 94US-00340426.
 PR (GEO) GEN HOSPITAL CORP.
 XX De La Monte S, Wanda JR;
 WPI, 1996-259865/26.
 N-PSDB; AAT27738.
 XX
 PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
 also NTP DNA and protein sequences used in gene and anti:sense therapy.
 XX
 PS Claim 22; Page 171-172; 238pp; English.
 XX
 CC A method for detecting the presence of neural thread protein (NTP) having
 a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
 comprises (a) contacting a sample from a human subject that is suspected
 of containing the NTP with at least one molecule capable of binding to
 the protein; and (b) detecting any of the molecule bound to the protein.
 The binding molecule is selected from an antibody free of natural
 impurities, a monoclonal antibody or a binding fragment of either of
 these. The method may be used for diagnosing the presence of Alzheimer's
 disease, neuroectodermal tumours and a malignant astrocytoma in a human
 XX
 SQ Sequence 397 AA;

Query Match 69.6%; Score 1415.5; DB 2; Length 397;
 Best Local Similarity 74.6%; Pred. No. 1.7e-135;
 Matches 285; Conservative 10; Mismatches 44; Indels 43; Gaps 7;
 QY 1 MEFSLLPLRLCNGAISAHRLNRLPGSSDSPASAPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLPLRLCNGAISAHRLNRLPGSSDSPASAPVAGITGCTHARLILYFFLVEMEF 60
 QY 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCP 110
 DB 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCP 110
 QY 111 WSPPELKQSTCLSLPKCDYRAAAYVGLFELFELHRCPTLTQDEVQWCHSSLOBSPE 170
 DB 111 WSPPELKQSTCLSLPKCDYRAAAYVGLFELFELHRCPTLTQDEVQWCHSSLOBSPE 170
 QY 171 ----IKHPPASQVAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWNLGSLQPLP 226
 DB 171 SSILPQPP-----KVAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWNLGSLQPLP 226
 QY 227 PGKLFSCPSLLSSDYRRPPRLANFVFLVEMGFTWFAFLILISGCDLPASASQAGIT 278
 DB 227 PGKLFSCPSLLSSDYRRPPRLANFVFLVEMGFTWFAFLILISGCDLPASASQAGIT 278
 QY 279 SASQAGITGVSHHARLIFNFCLEFEMESHVSTQAGVQWNLGSLQPLPPGKLFSCPSLL 338
 DB 282 --PKVLGLQDVTPTARPIFNFCLEFEMESHVSTQAGVQWNLGSLQPLPPGKLFSCPSLL 339
 QY 339 SSWDYGHLPHPANFCIFIRGG 360
 DB 340 SSWDYGHLPHPANFCIFIRGG 361

RESULT 12
 ID AAR95913
 XX AAR95913 standard; protein; 381 AA.
 AC AAR95913;
 XX
 DT 18-DEC-2001 (first entry)

XX Novel human secreted protein #726.
DE Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX Homo sapiens.
XX WO200179449-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US008656.
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX Claim 20; Page 264-265; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention
XX Sequence 381 AA;
Query Match 45.6%; Score 928; DB 4; Length 381;
Best Local Similarity 55.9%; Pred. No. 1e-85;
Matches 223; Conservative 27; Mismatches 101; Indels 48; Gaps 14;
QY 4 SLLPLRLCNGAISAHNRNLRPGSSDSPASAPVAGITGMCTHARLILYFFVLEHFLV 63
DB 4 SLLPLRLCNGAILAHNCNLCSGSSDSPASASQVTGKCHHTQLI-FVFLVEMGFHHI 62
QY 64 GAGLEPLTSDPSVSASQARYTG--HARLCLANFCGRNRVSLMCPFW----- 112
DB 63 AQAGLELLTSDPTL-ASQSAGI-TGVNHHAWLFF--FCSRDVSLCYPGWSRVAXSRIT 118
QY 113 --SPELKQSTCLSLPKCWDRRAAV--PGLFILFLRHRCTTLTQDEVQWCDHSSLQP--- 166
DB 119 ATSPGLKXKXACFLSSRDYRHVPHPGNFCIF-----GRDEVSPC-----WPGWF 164
QY 167 STPEIKHPASASQVAGTKDMHHYTW----LIPFIFNLRQSLNSVTQAGVQWNRGLSL 222
DB 165 XTPDLRYPPASASQSAEIIIGVSHHTWPQSVFLFLNLFIYLRWLSDSVAQARVQRDLGSL 224
QY 223 QPLPGFKLPSCFSLSSWDYR--PRLANFVFLVEMGFTHFARLILISGCDLPASAS 281
DB 225 QAPPFRFKPFCLSLPSSWDYRRPPPPHPANFFVFLVETGTVLARRVLISXPRDLPASAS 284

QY 282 QSAGITGVSHHARLIFNFCLEFEMESHVSQTQAGVQWPNLGLSQPLPGLKRFSCISLPSSW 341
DB 285 QSAGITGVSHHARLIFNFP--FETGTHSVTAAVQWYVTTIGSLQRTPELXKSSHLILTSNW 342
QY 342 DYGHLPHPAN-----FCIFIRGGVSPYLSGWSQTPDLR 375
DB 343 DYRCTPPCPNPLFIYLFYFHRDEGLSCFCGWSXTPELX 381
RESULT 13
AAU32610
ID AAU32610 standard; protein; 382 AA.
XX AC AAU32610;
XX 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #3101.
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX Homo sapiens.
XX WO200179449-A2.
XX 25-OCT-2001.
XX 16-APR-2001; 2001WO-US008656.
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX Claim 20; Page 637; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention
XX Sequence 382 AA;
Query Match 45.6%; Score 927.5; DB 4; Length 382;
Best Local Similarity 55.8%; Pred. No. 1.1e-85;
Matches 223; Conservative 27; Mismatches 101; Indels 49; Gaps 14;
QY 4 SLLPLRLCNGAISAHNRNLRPGSSDSPASAPVAGITGMCTHARLILYFFVLEHFLV 63
DB 4 SLLPLRLCNGAILAHNCNLCSGSSDSPASASQVTGKCHHTQLI-FVFLVEMGFHHI 62

QY 64 GOAGLELPTSDPSVSASQARYRTG--HHARLCLANFCGRNRVSLMCPWS- 113
 Db 63 AQAGLELLTSDPTL-ASQSAGI-TGVNHHAWLFF--FCSRDVSLCYPGWGRVAXSRIT 118
 QY 114 ----PELKQSTCLSLPKCWDYRAAV-PGLFILFLRHRCPRTLQDEVQWCHDSSLQP-- 166
 Db 119 ATSAPGLKXKXACFSLPSSRDYRHPHPCNFCIF-----GRDEVSPC-----WPGW 164
 QY 167 -STPEIKHPPASASQVAGTKDHHYTW-----LIFIFINFLRQSLNSVTOAGVQWRNLGS 221
 Db 165 FXTDLRYPPASASQSAEIIQVSHHTWQVEVFLNLFILYLRWSLDSVAQARVQRDLGS 224
 QY 222 LQPLPGRKLFSCPSLLSSWDYRR--PRLANFVFLVEMGFTMFARLILISGCDLPASA 280
 Db 225 LQAPPRFKPFCLSPSSWDYRRPPHPANFFVETGTVLARRVLISXPRDLASA 284
 QY 281 SOSAGITGVSHHARLIFNFCLEMESHVSVTQAGVQWPNLGSLOPLPPGLKRFCSCLSPSS 340
 Db 285 SOSAGITGVSHHARLIFNFCLEMESHVSVTQAGVQWPNLGSLOPLPPGLKRFCSCLSPSS 342
 QY 341 WDYGHLPPHPAN-----FCIFIRGVSPYLSGWSQTPDLR 375
 Db 343 WDYRCTPPCPNLFYLFYFHRDEGSLCCPGWSXTPELK 382

RESULT 14
 AAU31818
 ID AAU31818 standard; protein; 382 AA.
 AC AAU31818;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2309.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 513; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemia.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 382 AA;
 Query Match 45.6%; Score 927.5; DB 4; Length 382;
 Best Local Similarity 55.8%; Pred. No. 1.1e-85;
 Matches 223; Conservative 27; Mismatches 101; Indels 49; Gaps 14;
 QY 4 SLLPRLCNGAISHRNLRLLPGSSDSPASAPVAGITGMCTHARLILYFLVEMEPLHV 63
 Db 4 SLLPRLCNGAILAHCLNCLSGSSDSPASASQVITGKCHHTQLI-FVFLVEMGFHHI 62
 QY 64 GOAGLELPTSDPSVSASQARYRTG--HHARLCLANFCGRNRVSLMCPWS- 113
 Db 63 AQAGLELLTSDPTL-ASQSAGI-TGVNHHAWLFF--FCSRDVSLCYPGWGRVAXSRIT 118
 QY 114 ----PELKQSTCLSLPKCWDYRAAV-PGLFILFLRHRCPRTLQDEVQWCHDSSLQP-- 166
 Db 119 ATSAPGLKXKXACFSLPSSRDYRHPHPCNFCIF-----GRDEVSPC-----WPGW 164
 QY 167 -STPEIKHPPASASQVAGTKDHHYTW-----LIFIFINFLRQSLNSVTOAGVQWRNLGS 221
 Db 165 FXTDLRYPPASASQSAEIIQVSHHTWQVEVFLNLFILYLRWSLDSVAQARVQRDLGS 224
 QY 222 LQPLPGRKLFSCPSLLSSWDYRR--PRLANFVFLVEMGFTMFARLILISGCDLPASA 280
 Db 225 LQAPPRFKPFCLSPSSWDYRRPPHPANFFVETGTVLARRVLISXPRDLASA 284
 QY 281 SOSAGITGVSHHARLIFNFCLEMESHVSVTQAGVQWPNLGSLOPLPPGLKRFCSCLSPSS 340
 Db 285 SOSAGITGVSHHARLIFNFCLEMESHVSVTQAGVQWPNLGSLOPLPPGLKRFCSCLSPSS 342
 QY 341 WDYGHLPPHPAN-----FCIFIRGVSPYLSGWSQTPDLR 375
 Db 343 WDYRCTPPCPNLFYLFYFHRDEGSLCCPGWSXTPELK 382
 RESULT 15
 AAU32707
 ID AAU32707 standard; protein; 382 AA.
 XX
 AC AAU32707;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3198.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy.
PS Claim 20; Page 652; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 382 AA;

Query Match 45.6%; Score 927.5; DB 4; Length 382;
Best Local Similarity 55.8%; Pred. No. 1.1e-85;
Matches 223; Conservative 27; Mismatches 101; Indels 49; Gaps 14;

QY 4 SLLPLECNGAISAHNRNLPGSSDSPASAPVAGTCMCTHARLILYFFLVEHFLHV 63
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
4 SLLPLECNGAILAHNCNLCSGSDSPASASQVTGKCHHTQLI-EVFLVEMGFHHI 62
QY 64 GAGLELPTSDPSVSASQARVGTG--HHAELCLANFCGRNRVSLMCPSPWS----- 113
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
63 AQAGLELLTSDFTL-ASQAGI-TGVNHWLFF--FCSDTVSLCYPGNSRVAXSRIT 118
QY 114 ----PELKOSTCLSLPKQDYRAAV-PGLFILFLRHRCPRTLQDEVQWCDHSSLP-- 166
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
119 ATSAPGLKXKXACFLPSSRDYRHPVPHGNCIF-----GRDEVSPC-----WPGW 164
QY 167 -STPEIKHPASQVAGTKDMHHTW----LIFIFNPLRQSLNSVTOAGVQWRNLGS 221
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
165 FXTDPLRYPPASASQSAEIIQVSHHTWQVEFLFLMLFYLRWSLDSVAQARVQRDLGS 224
QY 222 LQPLPGRKLFSCPSLSSWDYR-PPRLANFVFLVEMGFTMEARLILISGCDLPASA 280
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
225 LQAPPRFPKFCCLPSSWDYRPPHPANFVFLVETGFTVLARRVLISPRDLPASA 284
QY 281 SQSAGITGVSHHARLIFNFCLEFEMESHVTOAGVQWPNLGSQPLPPGLKRFSCLSLPS 340
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
285 SQSAGITGVSHHTRLI-FNF--FETGTHSVTAAVQWYTIQSLQPRTPELKXSSHLILTSN 342
QY 341 WDYGHLPHPAN-----FCIFIRGGVSPYLSQWSQTPDLR 375
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
343 WDYRCTPPCPNLIYFLFYFHRDEGSLCCPGNSKTXPELK 382

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Run on: September 15, 2005, 22:16:29 ; Search time 810 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 7389322 seqs, 331285599 residues

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	100.0	1442	9 US-09-964-666-1	Sequence 1, Appli
2	2034	100.0	1442	9 US-09-964-412-1	Sequence 1, Appli
3	2034	100.0	1442	10 US-09-964-667-1	Sequence 1, Appli
4	2034	100.0	1442	10 US-09-964-668-1	Sequence 1, Appli
5	2034	100.0	1442	10 US-09-964-678A-1	Sequence 1, Appli
6	2034	100.0	1442	14 US-10-146-130-1	Sequence 1, Appli
7	2034	100.0	1442	14 US-10-092-934-1	Sequence 1, Appli
8	2034	100.0	1442	14 US-10-153-334-53	Sequence 53, Appli
9	2034	100.0	1442	14 US-10-198-069-48	Sequence 48, Appli
10	2034	100.0	1442	15 US-10-198-070-125	Sequence 125, App
11	2034	100.0	1442	19 US-10-755-889-409	Sequence 409, App
12	2034	100.0	1442	21 US-10-910-173-1	Sequence 1, Appli
13	1787	87.9	1418	9 US-09-964-666-4	Sequence 4, Appli
14	1787	87.9	1418	9 US-09-964-412-4	Sequence 4, Appli
15	1787	87.9	1418	10 US-09-964-667-4	Sequence 4, Appli
16	1787	87.9	1418	10 US-09-964-678A-4	Sequence 4, Appli
17	1520	74.7	1381	9 US-09-964-666-3	Sequence 3, Appli
18	1520	74.7	1381	9 US-09-964-412-3	Sequence 3, Appli
19	1520	74.7	1381	10 US-09-964-667-3	Sequence 3, Appli
20	1520	74.7	1381	10 US-09-964-678A-3	Sequence 3, Appli
21	964.5	47.4	75252	13 US-10-087-192-904	Sequence 904, App
22	901	44.3	33362	19 US-10-388-838-36	Sequence 36, Appli
23	892.5	43.9	92638	19 US-10-450-836-3	Sequence 3, Appli
24	871.5	42.8	103574	22 US-10-756-149-2307	Sequence 2307, Ap
25	870	42.8	193691	20 US-10-719-993-6768	Sequence 6768, Ap
26	870	42.8	187660	20 US-10-719-993-6765	Sequence 6765, Ap
27	863.5	42.5	110096	9 US-09-880-107-1542	Sequence 1542, Ap
28	861.5	42.4	21666	18 US-10-052-482-208	Sequence 208, App
29	858	42.2	126001	17 US-10-175-492-13	Sequence 13, Appli
30	857	42.1	32865	13 US-10-087-192-964	Sequence 964, App
31	851.5	41.9	3379	10 US-09-964-821B-3	Sequence 3, Appli
32	851.5	41.9	3379	16 US-10-268-332-3	Sequence 3, Appli
33	851.5	41.9	28953	20 US-10-775-965-3	Sequence 3, Appli
34	851.5	41.9	28953	20 US-10-719-993-6811	Sequence 6811, Ap
35	848.5	41.7	15783	10 US-09-764-872-700	Sequence 700, App
36	848	41.7	61103	13 US-10-087-192-58	Sequence 58, Appli
37	846	41.6	124990	20 US-10-684-422-156	Sequence 156, App
38	841.5	41.4	40645	9 US-09-818-656A-3	Sequence 3, Appli
39	841.5	41.4	40645	13 US-10-216-441-3	Sequence 3, Appli
40	841.5	41.4	40645	22 US-10-961-230-3	Sequence 3, Appli
41	840	41.3	27148	9 US-09-764-860-1046	Sequence 1046, Ap
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44	840	41.3	74234	13 US-10-087-192-1120	Sequence 316, App
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ALIGNMENTS

RESULT 1
US-09-964-666-1
; Sequence 1, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC

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; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-666-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-380-203-2 (1-375) x US-09-964-666-1 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTTTGTCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 74
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValIalaGlylle 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGCAGTAGCTGGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGAGTGTGACCCACCGCTCGGCTAAATTTTGTATTTTGTATAGAGATGGAGTTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCATGTTGGTCAGGCTGGTCTCGAATCCCGACCTCAGATGATCCCTCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGCTAGATACAGGACTGGCCACCATGCGCGCTCTGCTGGCTAAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTyrSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAAACAGGGTTTCACTGATGTCCTCAAGCTGCTCTCCTGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTyrAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCTCCCAAGTGTGGGATTACAGCGGTGACGCGTGGCTGGCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTyrCysAsp 160
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QY 181 ValIalaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCACTACACCTGGCTAAATTTTATTTTATTTTAAAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTCAACCGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerSerLeuLeuSerSer 240
Db 675 TCACGTGCAACCTCTGCTCCCGGTTCAAGTTATTTCTCTGCCCCAGGCTCTCTGAGTAGC 734
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QY 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
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QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCATGGCAATCTCGGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACGTGCAACCTCTGCTCCCGGCTCAAGCGATTCTCTGCTCAGCCTCCCAAAGCAGC 1034
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Db 1035 TGGGATTACGGGCACCTGCCACCAACCCCGCTAAATTTTGTATTTTCAATAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTyrPheSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTCTCAGGCTGGTCTCAAACTCTCGACCTCAGG 1139

RESULT 2
US-09-964-412-1
; Sequence 1, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.

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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1139
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-412-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-380-203-2 (1-375) x US-09-964-412-1 (1-1442)

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QY	21	AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle	40
DB	75	ACCTCCGCTCCGCGTTCAGCGATCTCTGCTCAGCTCCCGCTCCCGCTCAGCTGGATT	134
QY	41	ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe	60
DB	135	ACAGGATGTGCACCCAGCTCGGCTAATTTTGTATTTTATTTTATTTAGTAGAGTGGATT	194
QY	61	LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla	80
DB	195	CTCCATGTGGTCAGCTGGTCTCGAATCTCCGACCTCAGATGATCCCTCCGCTCGGCC	254
QY	81	SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys	100
DB	255	TCCCAAGTGTAGATACAGGACTGGCCACCAATGCCCCGCTCTGCTGGCTAATTTTGT	314
QY	101	GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr	120
DB	315	GGTAGAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTCAGCTCAAGCAGTCCACC	374
QY	121	CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle	140
DB	375	TGCCTCAGCTCCCAAGTGTGGGATTACAGCGGTGCGAGCTGCGCTGCGCTTTTAT	434
QY	141	LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp	160
DB	435	TTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGATGAGTGCAGTGGTGTAT	494
QY	161	HisSerSerLeuGlnProSerThrProGluIleLysHisProAlaSerAlaSerGln	180
DB	495	CACAGCTCACTCAGCGCTTCAACTCTCTGAGATCAAGCATCTCTGCTCAGCTCCCAA	554
QY	181	ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsn	200
DB	555	GTAGCTGGGACCAAGACATGACCACTACACTCAGCTGGCTAATTTTATTTTAT	614
QY	201	PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly	220
DB	615	TTTTTGTAGACAGATCTCAACTCTGTCCACCGAGTGGAGTGCAGTGGCGCAATCTGGC	674
QY	221	SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer	240

DB	675	TCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTCTCTGCCCCAGCCTCTCTGAGTAGC	734
QY	241	TrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly	260
DB	735	TGGGACTACAGCGGCCCCACACCGCTAGCTAATTTTGTATTTTATTTAGTAGATGGGG	794
QY	261	PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla	280
DB	795	TTACCATGTTCCCGCAGGTGATCTCTGACCTTGATCTGCTGCTGCTGCTGCTGCTGCTG	854
QY	281	SerGlnSerAlaGlyIleThrGlyValSerHisAlaArgLeuIlePheAsnPheCys	300
DB	855	TCCCAAGTGTGGATTACAGCGCTGAGCCACCGCGCTTATTTTATTTTATTTTAT	914
QY	301	LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly	320
DB	915	TTGTTTGAATGGAATCTCACTCTGTACCCAGGCTGGAGTGCATGGCCAAATCTCGGC	974
QY	321	SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer	340
DB	975	TCACTGCAACCTCTGCTCCCGGGCTCAAGCGATTCTCTGCTCAGCTCCCAAGCAGC	1034
QY	341	TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly	360
DB	1035	TGGGATTACGGGCACCTGCCACCAACCCCGCTAATTTTGTATTTTATTTTATTTAGAGCGGG	1094
QY	361	ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg	375
DB	1095	GTTCACCATATTTGTGAGGTGGTCTCAAACTCTCGACCTCAGG	1139

RESULT 3
US-09-964-667-1
; Sequence 1, Application US/09964667
; Publication No. US20030033621A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wanda, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,667
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 15..1139
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-964-667-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-380-203-2 (1-375) x US-09-964-667-1 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACCGC 74

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
DB 75 AACCTCCGCTCCCGGGTTCAGAGCAATCTCTCGCTCAGCCTCCCGAGTAGCTGGGATT 134

QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
DB 135 ACAGGATGTGCACCCAGCTCGGCTAATTTGTATTTTATTTAGTAGAGATGGAGTTT 194

QY 61 LeuHisValGlyGlnAlaGlyLeuLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
DB 1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAATTTTGTATTTTTCATTAGAGCGGG 1094

QY 361 ValSerProTyrLeuSerGlyTyrSerGlnThrProAspLeuArg 375
DB 1095 GTTTCACCATATTTTGCAGGCTGGTCTCAAACTCCTGACCTCAGG 1139

RESULT 4
US-09-872-968-1
; Sequence 1, Application US/09872968
; Publication No. US20030050262A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872, 968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-968-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-380-203-2 (1-375) x US-09-872-968-1 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACCGC 74

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
DB 75 AACCTCCGCTCCCGGGTTCAGAGCAATCTCTCGCTCAGCCTCCCGAGTAGCTGGGATT 134

QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
DB 135 ACAGGATGTGCACCCAGCTCGGCTAATTTGTATTTTATTTAGTAGAGATGGAGTTT 194

QY 61 LeuHisValGlyGlnAlaGlyLeuLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
DB 1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAATTTTGTATTTTTCATTAGAGCGGG 1094

QY 361 ValSerProTyrLeuSerGlyTyrSerGlnThrProAspLeuArg 375
DB 1095 GTTTCACCATATTTTGCAGGCTGGTCTCAAACTCCTGACCTCAGG 1139
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Db 375 TGCCTCAGCGCTCCCAAGTGTGGGATTACAGCGGTGACGGCTGCTGGCGCTTTTATT 434
Qy 141 LeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTTATTTTTTTTAAAGACACAGGTGTCCCACTCTTACCAGAGTGAAGTGCAGTGGTGTGAT 494
Qy 161 HisSerSerLeuGlnProSerThrProGluLeuLeuHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGACGCTTTCAACTCTCTGAGATCAAGCATCTCTGCTCAGCGCTCCCAA 554
Qy 181 ValAlaGlyThrIlysAspMetHisHisIstYrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACCTGCTTAATTTTTTATTTTTTAT 614
Qy 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTACCCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
Qy 221 SerLeuGlnProLeuProGlyPheLeuLeuPheSerCysProSerSerLeuLeuSerSer 240
Db 675 TCACGTCAACCTCTGCTCCCGGTTCAAGTTATTCTCTGCGCCAGCGCTCTGAGTAGC 734
Qy 241 TrpAspTyrArgArgProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGCGCCACCGCTAGCTAATTTTTTTGTATTTTTTTAGTAGAGATGGGG 794
Qy 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280
Db 795 TTCACCATGTTCCGACAGGTGATCTTGATCTCTGACCTTGTGATCTGCTCGCTCGGCC 854
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Db 855 TCCCAAGTGTGGGATTACAGCGGTGACCGCCAGCGCTTATTTTATTTTGT 914
Qy 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTGAATGGAATCTCACTCTGTACCCAGGCTGGAGTGAATGGCAATCTCGGC 974
Qy 321 SerLeuGlnProLeuProGlyLeuIlysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACGTCAACCTCTGCTCCCGGCTCAAGCGATCTCTGCTCAGCGCTCCCAAGCAGC 1034
Qy 341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGCAGCTGCCACACACACCGCTTATTTTGTATTTTCAATTAGAGCGGG 1094
Qy 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTGTGAGGCTGGTCTCAAACTCTCTGACCTCAGG 1139

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RESULT 5

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US-09-964-678A-1
; Sequence 1, Application US/09964678A
; Publication NO. US2003066097A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
; TITLE OF INVENTION: Effective for the Treatment or Prevention of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4370002
; CURRENT APPLICATION NUMBER: US/09/964,678A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/380,203
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US98/03685
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/038,908
; PRIOR FILING DATE: 1997-02-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1442

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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AD7c-NTP CDNA
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
; OTHER INFORMATION:
US-09-964-678A-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-380-203-2 (1-375) x US-09-964-678A-1 (1-1442)
Qy 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTTGGCTCTTGTGGCCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 74
Qy 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCGCTCCCGAGTAGCTGGATT 134
Qy 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGCATGTGCACCGCTCGGCTAATTTTGTATTTTTTTTATTTAGTAGAGATGGAGTT 194
Qy 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCCATGTTGGTCAGGCTGGTCTCGAATCTCCGACTCAGATGATCCCTCCGCTCTCGGCC 254
Qy 81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAGTGTGTAGATACAGGACTGGCCACCATGCCGCTCTGCTGGCTAATTTTGT 314
Qy 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuIlysGlnSerThr 120
Db 315 GGTGAAAACAGGGTTTCACTGATGTGCCCAAGTGTCTCTCAGCTCAAGCAGTCCACC 374
Qy 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCGCTCCCAAGTGTGGGATTACAGCGGTGACGGCTGCGCTGCGCTTTTATT 434
Qy 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTTATTTTTTTTAAAGACACAGGTTGCCACTCTTACCAGGATGAAGTGCAGTGGTGTGAT 494
Qy 161 HisSerSerLeuGlnProSerThrProGluLeuIlysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGACGCTTTCAACTCTCTGAGATCAAGCATCTCTCTGCTCAGCGCTCCCAA 554
Qy 181 ValAlaGlyThrIlysAspMetHisHisIstYrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACCTGCTTAATTTTTTATTTTTTAT 614
Qy 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTACCCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
Qy 221 SerLeuGlnProLeuProGlyPheLeuLeuPheSerCysProSerSerLeuLeuSerSer 240
Db 675 TCACGTCAACCTCTGCTCCCGGTTCAAGTTATTCTCTGCGCCAGCGCTCTGAGTAGC 734
Qy 241 TrpAspTyrArgArgProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGCGCCACCGCTAGCTAATTTTTTTGTATTTTTTTAGTAGAGATGGGG 794
Qy 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280

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Db 795 TTCACCATGTTCCGACGGTTGATCTTGATCTCTGACCTTGATCTGCCTCGCTCGGCC 854
Qy 281 SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePheAsnPheCys 300
Db 855 TCCCAAAGTGCTGGGATTACAGCGGTGAGCCACCGCCGGCTTATTTTAAATTTTGT 914
Qy 301 LeuPheGluMetGlnSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTTGAATGAAATCTCACTCTGTATACCCAGGCTGGAGTGCAATGGCCAAATCTCGGC 974
Qy 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACCTGCAACCTCTGCCTCCCGGCTCAAGCGATTCTCTGTCTAGCCCTCCCAAGCAGC 1034
Qy 341 TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
Qy 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTGAGGCTGGTCTCAAACTCTCGACCTCAGG 1139

RESULT 6

US-10-146-130-1
; Sequence 1, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-146-130-1

Alignment Scores:

Pred. No.: 7.83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-380-203-2 (1-375) x US-10-146-130-1 (1-1442)

Qy 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTGTGTTGCCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACCGC 74
Qy 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGCTCCCGGTTCAAGCGATTCTCTGCTCCTAGCCTCCCGCTCAGTAGTGGATT 134
Qy 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGATGTGCACCCACCGCTCGGCTAAATTTTGTATTTTCTAGTAGAGATGGAGTTT 194
Qy 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCATGTGGTCAGGCTGTCTCGAACTCCCGACCTCAGATGATCCCTCCGCTCGGCC 254
Qy 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGCTAGATACAGGACTGGGCCACCATGTCGCGGCTCTGCTGCTAATTTTGT 314

RESULT 7

US-10-092-934-1
; Sequence 1, Application US/10092934
; Publication No. US200300054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1

Qy 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAAACAGGGTTTCACTGATGTGCCAAAGCTGCTCTCTGAGCTCAAGCAGTCCAC 374
Qy 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCCCTCCCAAAGTGTGGGATTACAGCGGTGACCGCTGCGCTGCGCTTTTATT 434
Qy 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTGCAGTGGTGTGAT 494
Qy 161 HisSerSerLeuGlnProSerThrProGluLysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGCAGCCTTCAACTCTGAGATCAAGCATCTCTCTGCTGCTCAGCCTCCCAA 554
Qy 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCATACACCTGGCTAATTTTATTTTATTTTATTTTAT 614
Qy 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTGACACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
Qy 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
Db 675 TCACCTGCAACCTCTGCCTCCCGGTTCAAGTTATTTCTCTGCGCCAGGCTCTCTGAGTAGC 734
Qy 241 TrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGGCGCCACCGCTAGCTAATTTTGTATTTTGTATTTTGTAGTAGATGGG 794
Qy 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
Db 795 TTCACCATGTTTCGCCAGGTTGATCTTGATCTCTGACCTTGTGATCTGCTCGCTCGGCC 854
Qy 281 SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePheAsnPheCys 300
Db 855 TCCCAAAGTGCTGGGATTACAGCGGTGAGCCACCGCGGCTTATTTTAAATTTTGT 914
Qy 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTTGAATGGAATCTCACTCTGTACCCAGGCTGGAGTGCAATGGCCAAATCTCGGC 974
Qy 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACCTGCAACCTCTGCCTCCCGGCTCAAGCGATTCTCTGCTCAGCCTCCCAAGCAGC 1034
Qy 341 TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGGCACCTGCCACACCCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
Qy 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTGAGGCTGGTCTCAAACTCTCGACCTCAGG 1139

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; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-934-1

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-380-203-2 (1-375) x US-10-092-934-1 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 15 ATGGAGTTTTCGCTCTTGTTCGCCAGGCTGGAGTGCATTCAGTGGCGCAATCTCAGCTCACCGC 74
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyLe 40
DB 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTCGCTCAGGCTCCCGAGTGGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyPhePheLeuValGluMetGluPhe 60
DB 135 ACAGGATGTGACCCACCGCTCGGCTAATTTGTATTTTTTTTAGTAGATGGAGTTT 194
QY 61 LeuHisValGlyAlaGlyLeuLeuProThrSerAspProSerValSerAla 80
DB 195 CTCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATCCCTCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
DB 255 TCCAAAGTGCTAGATACAGGACTGGCCACCATGCGCGCTCTCGCTGGCTAAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLeuGlnSerThr 120
DB 315 GGTAGAAAACAGGGTTTCACTGATGTGCCACAGCTGGTCTCTGAGCTCAAGCATCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyArgAlaAlaValProGlyLeuPheIle 140
DB 375 TGCCTCAGCCTCCCAAAGTGTGGGATTACAGCGGTGCAGCGCTGCCTGGCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
DB 435 TTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTGCATGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleHisProProAlaSerAlaSerGln 180
DB 495 CACAGCTCACTGAGCCITCAACTCTGTAGATCAAGCATCTCTCGCTCAGCCTCCCAA 554
QY 181 ValAlaGlyThrLysAspMetHisIstYrThrTrpLeuIlePheIlePheAsn 200
DB 555 GTAGCTGGGACCAAGACATGCACCATACACTCGCTGCTAATTTTATTTTATTTTAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
DB 615 TTTTGTAGACAGAGTCTCAACTCTGTACCCAGGCTGGAGTGCATGTCGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
DB 675 TCACCTGAACCTCTGCTCCCGGTTCAAGTTATTCTCTCGCCCGAGCTCTCAGTAGC 734
QY 241 TrpAspTyArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
DB 735 TGGGACTACAGGCGCCACACAGCTAGCTAATTTTGTATTTTATTTAGTAGATGGG 794
QY 261 PheThrMetPheAlaArgLeuLeuIleSerGlyProCysAspLeuProAlaSerAla 280

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QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAGTGTAGATACAGGACTGGCCACCAATGCCCGCTCTGCTGGCTAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGCTCTCTGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCCTCCCAAGTGTGGGATTACAGCGGTGCAGCGTGCCTGGCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTAAAGACACAGGTGTCCCACTCTTACCACGAGTGAAGTGCAGTGGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluLeuLysHisProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGAGCCTTCAACTCTCTGAGATCAAGCATCTCTCTGCTCAGCCTCCCA 554
QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACACCTGGCTAATTTTATTTTATTTTAAAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTACCCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
Db 675 TCACATGCACCTCTGCTCCCGGTTCAAGTTATTCTCTGCCAGCCTCTCTGAGTAGC 734
QY 241 TrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGCGCCACACCGCTAGCTAATTTTGTATTTTGTAGAGATGGGG 794
QY 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
Db 795 TTCACCATGTTCCGACGGTGTGATCTTGACCTTGAGATCTGCTCCCTCGCGCC 854
QY 281 SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePheAsnPheCys 300
Db 855 TCCCAAGTGTGGGATTACAGCGGTGAGCCACCGCCCGCTTATTTTAAATTTTGT 914
QY 301 LeuPheGluMetGlnSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTGAAATGGAATCTCACTCTGTATCCAGGCTGGAGTGAATGGCCAAATCTCGGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACTGCAACCTCTGCTCCCGGCTCAAGCGATTCTCTGTCTCAGCCTCCCAAGCAGC 1034
QY 341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGGACCTGCCACACACCCCGCTAATTTTGTATTTTCAATAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGG 1139
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RESULT 9

US-10-198-069-48

; Sequence 48, Application US/10198069

; Publication No. US20030096756A1

; GENERAL INFORMATION:

; APPLICANT: AVERBACK, PAUL

; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER

; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 59003.000009

; CURRENT APPLICATION NUMBER: US/10/198,069

; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,161

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; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-198-069-48

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-380-203-2 (1-375) x US-10-198-069-48 (1-1442)
QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTTGTGTCGCCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 74
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCGCTAGTGGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGCATGTGCACCCACGCTCGGCTAATTTTGTATTTTATTTTATTTAGTAGAGATGGAGTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspProSerValSerAla 80
Db 195 CTCATGTGTGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCGCTCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAGTGTGTAGATACAGGACTGGCCACCACTGCGCTGCTGCTGGCTAAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAAACAGGGTTTCACTGATGTGCCCAAGCTGCTCTCTGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCCTCCCAAGTGTGGGATTACAGCGGTGCAGCGTGCCTGGCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTAAAGACACAGGTGTCCCACTCTTACCACGAGTGAAGTGCAGTGGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluLeuLysHisProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGAGCCTTCAACTCTCTGAGATCAAGCATCTCTCTGCTCAGCCTCCCA 554
QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACACCTGGCTAATTTTATTTTATTTTAAAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTGTCACCGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
Db 675 TCACATGCACCTCTGCTCCCGGTTCAAGTTATTCTCTGCCAGCCTCTCTGAGTAGC 734
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QY 241 TrpAspTyrArgArgProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
DB 735 TGGAGCTACAGGCGCCACACCGCTAGCTAATTTTGTATTTTAGTAGAGATGGG 794
QY 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280
DB 795 TTCACCATGTTCGCCAGGTGATCTTGATCTCGGACCTTGATCTGCTCGCTCGGCC 854
QY 281 SerGlnSerAlaGlyThrGlyValSerHisHisAlaArgLeuLeuPheAsnPheCys 300
DB 855 TCCCAAAGTGTGGGATACAGCGTGGAGCCACCGCCGGCTAATTTTAAATTTTGT 914
QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
DB 915 TTGTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGAATGGCAATCTCGGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
DB 975 TCAGTCAACCTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCAGCCTCCCAAGCAGC 1034
QY 341 TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysLeuPheLeuArgGlyGly 360
DB 1035 TGGGATTACGGGACCTGCCACACCGCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
DB 1095 GTTTCACCATATTTGTACGGCTGGTCTCAAACTCTGACCTCAGG 1139

RESULT 10

US-10-198-070-125
; Sequence 125, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-198-070-125

Alignment Scores:

Pred. No.: 7.83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-380-203-2 (1-375) x US-10-198-070-125 (1-1442)

QY 1 MetGluPheSerLeuLeuProArgLeuGluCysAsnGlyAlaLeuSerAlaHisArg 20
DB 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGAATGGCGCAATCTCAGCTCACCGC 74

RESULT 11

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
DB 75 AACCTCCGCTCCCGGTTCAAGCGATTTCTCTGCTCAGCCTCCCAAGTAGTGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuPhePheLeuValGluMetGluPhe 60
DB 135 ACAGCATGTGACCCAGCCTCGGCTAATTTTGTATTTTATTTTAGTAGAGATGGAGTTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAla 80
DB 195 CTCCATGTGGTCAGGCTGGTCTCGAACTCCCGACTCAGATGATCCCTCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
DB 255 TCCCAAAGTGTCTAGATACAGGACTGGCCACCATGCGCGCTCTGCTGGCTAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
DB 315 GGTAGAAAACAGGTTTCACTGATGTGCCCAAGCTGCTCTCTGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
DB 375 TGCCTCAGCTCCCAAGTGTGGGATTTACAGCGGTGACAGCTGCTGCTGCTTTTAT 434
QY 141 LeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
DB 435 TTATTTTTTAAAGACACAGGTGTCCTCACTCTTACCCAGGATGAAGTGCAGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluLeuLysHisProProAlaSerAlaSerGln 180
DB 495 CACAGCTCACTGCAGCTTCAACTCTGAGATCAAGCATCTCTCTGCTGCTCAGCCTCCCAA 554
QY 181 ValAlaGlyThrLysAspMetHisHisThrTrpLeuLeuPheIlePheLeuPheAsn 200
DB 555 GTAGCTGGGACCAAGACATGCACCATACCTGCTGGCTAATTTTATTTTATTTTAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
DB 615 TTTTGTAGACAGAGTCTCAACTCTCTCACCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
DB 675 TCAGTGCACCACTCTGCTCCCGGTTCAAGTTATTTCTCTGCCCGCCAGCTCTCTGAGTAGC 734
QY 241 TrpAspTyrArgArgProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
DB 735 TGGGACTACAGCGCCCAACACCGCTAGCTAATTTTGTATTTTGTAGTAGAGATGGGG 794
QY 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280
DB 795 TTCACCATGTTCCGCCAGGTTGATCTTGATCTCTGGACCTTGTGATCTGCTCGCTCGGCC 854
QY 281 SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuLeuPheAsnPheCys 300
DB 855 TCCCAAAGTGTGGGATTTACAGCGGTGAGCCACCGCCGGCTAATTTTAAATTTTGT 914
QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
DB 915 TTGTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGAATGGCAATCTCGGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
DB 975 TCAGTGCACCACTCTGCTCCCGGCTCAAGCGATTTCTCTGCTCAGCCTCCCAAGCAGC 1034
QY 341 TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheLeuArgGlyGly 360
DB 1035 TGGGATTACGGGACCTGCCACACCGCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
DB 1095 GTTTCACCATATTTGTACGGCTGGTCTCAAACTCTCTGACCTCAGG 1139

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US-10-755-889-409
; Sequence 409, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 409
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-409

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-380-203-2 (1-375) x US-10-755-889-409 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGGCAATCTCAGCTCACCGC 74
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValaIleGly 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGAATCTCTGCTCAGCTCCCGCAATGGGAT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGCAATGTCACCCAGCTCGGCTAATTTGTTATTTTGTAGTAGAGATGGAGTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAla 80
Db 195 CTCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGTAGATACAGGACTGGCCACCAATGCCGCTCTGCTGGCTAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTyrSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAACAGGGTTTCACTGATGTCGCCAAGCTGCTCTCCTGAGTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTyrAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCTCCCAAGTGTGGGATTAACAGCGTGCAGCGTGCCTGCTGCTGCTTTTAT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTyrCysAsp 160
Db 435 TTATTTTTTTTAAACACAGGTTGCCACTCTTACCAGGATGAGTGGAGTGGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTCAGCGCTTCAACTCTGAGATCAAGCATCTCTGCTCAGCTCCCA 554
QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePhePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACCTGGCTAATTTTATTTTATTTTAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpAsnLeuGly 220
Db 75 AACCTCCGCTCCCGGGTTCAAGCGAATCTCTGCTCAGCTCCCGCAATCTCAGCTCACCGC 74

US-10-755-889-409
; Sequence 409, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 409
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-409

Alignment Scores:
Pred. No.: 7,83e-197 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-380-203-2 (1-375) x US-10-755-889-409 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGGCAATCTCAGCTCACCGC 74
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValaIleGly 40
Db 75 AACCTCCGCTCCCGGGTTCAAGCGAATCTCTGCTCAGCTCCCGCAATGGGAT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGCAATGTCACCCAGCTCGGCTAATTTGTTATTTTGTAGTAGAGATGGAGTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAla 80
Db 195 CTCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGTAGATACAGGACTGGCCACCAATGCCGCTCTGCTGGCTAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTyrSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAACAGGGTTTCACTGATGTCGCCAAGCTGCTCTCCTGAGTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTyrAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCTCCCAAGTGTGGGATTAACAGCGTGCAGCGTGCCTGCTGCTGCTTTTAT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTyrCysAsp 160
Db 435 TTATTTTTTTTAAACACAGGTTGCCACTCTTACCAGGATGAGTGGAGTGGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTCAGCGCTTCAACTCTGAGATCAAGCATCTCTGCTCAGCTCCCA 554
QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePhePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGACCACTACCTGGCTAATTTTATTTTATTTTAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpAsnLeuGly 220
Db 75 AACCTCCGCTCCCGGGTTCAAGCGAATCTCTGCTCAGCTCCCGCAATCTCAGCTCACCGC 74
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QY 120 hrCysLeuSerLeuProLysCysTTPAspTyrArgAlaAlaValProGlyLeuPheI 140
Db 372 CTGGCTCAGCTCCCAAAGTGTGGATTACAGCGTGCACCGCGCTGGCCCTTTTAA 431
QY 140 leLeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
Db 432 TTTTATTTTTTAAGACACAGGTGTCCCACTCTTACCAGGATGAAGTGCAGTGGTGTG 491
QY 160 sPHisSerLeuGlnProSerThrProGluLeuLysHisProProAlaSerAlaSerG 180
Db 492 ATCACAGCTCACTGCAGCCTTCAACTCT-GAGATCAAGCATCTCTCTGCCTCAGCCTCC 550
QY 180 ln-ValAlaGlyThriLysAspMetHisHisTyrThrTrpLeuLephelePhe 199
Db 551 AAAGTAGCTGGGACCAAGACATGACCACTACCTGCTAAATTTTTTATTTTTT 610
QY 200 AnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
Db 611 AATTTTTTGAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGCGCAATCTT 670
QY 220 GlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSer 239
Db 671 GGCTCACTGCACACCTCTGCTCCCGGTTCAAGTTATTCTCTGCGCCAGCCTCCTGAGT 730
QY 240 SerTrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuValGluMet 259
Db 731 AGCTGGGACTACAGGCGGCCACACGCTAGTAAATTTTTTGTATTTTATGTAGTAGAGATG 790
QY 260 -GlyPheThrMetPheAlaArgLeuLeu- IleSerGlyProCysAspLeuProAlaS 279
Db 791 GGGTTTCAACCATGTTGCGCAGGTTGATGCTAGATCTCTTGACCTTGTATCTGCTGCT 850
QY 279 erAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis-AlaArgLeuIlePheAsn 298
Db 851 CGGCTCCCAAAGTGTGGATTACAGGACGTGACGCCACCGCCGCGCTATTTTTTAAT 910
QY 299 PheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsn 318
Db 911 TTTTGTGTTTGAATGAATCTCCTCCTGTACCCAGGCTGGAGTGCAATGGCCAAAT 970
QY 319 LeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuPro 338
Db 971 CTCGGCTCACTGCAACCTCTGCTCCCGGCTCAAGCGATCTCTGTCTCAGCCTCCCA 1030
QY 339 SerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheleArg 358
Db 1031 AGCAGCTGGGATTACGGGCACCTGCA-CCACACCCCGCTAAATTTTGTATTTTCATTAGA 1089
QY 359 GlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1090 GCGGGGGTTTACCATAATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGG 1140
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RESULT 14

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US-09-964-412-4
; Sequence 4, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-964-412-4
Alignment Scores:
Pred. No.: 1,08e-171 Length: 1418
Score: 1787.00 Matches: 363
Percent Similarity: 95.54% Conservative: 1
Best Local Similarity: 95.28% Mismatches: 11
Query Match: 87.86% Indels: 10
DB: 9 Gaps: 0
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QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 14 ATGGAGTTTCGCTCTTGTTCGCCAGGTGAGTGCATGGCGCAATCTCAGCTCACC GC 73
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProVal-AlaGlyI 40
Db 74 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCCAAGTAGGCTGGAT 133
QY 40 eThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPh 60
Db 134 TACAGGATGTCACAC-CACGCTCGGCTAAATTTTGTATTTTTTTTAGTAGAGATGAGTT 192
QY 60 eLeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAl 80
Db 193 TCTCCATGTTGGTCAGGCTGGTCTCGAACT-CCGACCTCAGATGATCTCTCCGCTCGGC 251
QY 80 aSerGlnSerAlaArgTyrArgThrGlyHisHisAlaArg-LeuCysLeuAlaAsnPheC 100
Db 252 CTCCCAAAGTCTAGATACAGGACTGAGCACCATGCGCGGCTCTGCTGGCTAAATTTT 311
QY 100 ysGlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerT 120
Db 312 GTGGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTCCAGCTCAAGCAGTCCA 371
QY 120 hrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheI 140
Db 372 CTGCTCAGCTCCCAAAGTGTGGGATTACAGCGTGCACCGCTGCTGGCCCTTTTAA 431
QY 140 leLeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
Db 432 TTTTATTTTTTAAAGACACAGGTGTCCCACTCTTACCAGGATGAAGTGCAGTGGTGTG 491
QY 160 sPHisSerLeuGlnProSerThrProGluLeuLysHisProProAlaSerAlaSerG 180
Db 492 ATCACAGCTCACTGCAGCCTTCAACTCT-GAGATCAAGCATCTCTCTGCCTCAGCCTCC 550
QY 180 ln-ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuLephelePhe 199
Db 551 AAAGTAGCTGGGACCAAGACATGACCACTACCTGCTAAATTTTTTATTTTTT 610
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QY 200 AsnPheLeuArgGlnSerLeuAenSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
Db 611 AATTTTGGAGACAGAGTCTCAACTGTGTCAACCCAGGCTGAGTGCAGTGGCGCAATCTT 670
QY 220 GlySerLeuGlnProLeuProGlyPheLeuPheSerCysProSerLeuLeuSer 239
Db 671 GGCTCACTGCAACTCTGCTCCCGGGTTCAAGTTATTTCTCTCCGCCCGCACTCTCGAGT 730
QY 240 SerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMet 259
Db 731 AGCTGGAGCTACAGGCGCCACACCGCTAGCTAAATTTTGTATTTTAGTAGAGATG 790
QY 260 -GlyPheThrMetPheAlaArgLeuLeuLeu-ileSerGlyProCysAspLeuProAlas 279
Db 791 GGGTTTTCACCATGTCGCCAGGTGTGATGCTAGATCTCTTGACCTTGTGATCTGCTGCT 850
QY 279 erAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis-AlaArgLeuLeuPheAsn 298
Db 851 CGGCTCTCCCAAGTGTGGGATTTACAGGACGTGACGCCCGCCCGGCTATTTTAAAT 910
QY 299 PheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsn 318
Db 911 TTTTGTGTGTTGAAATGGAAATCTCACTCTGTGTACCCAGGCTGAGTGCAGTGGCCAAAT 970
QY 319 LeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuPro 338
Db 971 CTGGCTCACTGCAACTCTGCTCCCGGGCTCAAGGATTTCTCTGTCTCAGCTCCCA 1030
QY 339 SerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheLeuArg 358
Db 1031 AGCAGCTGGGATTTACGGGACCTGCA-CCACACCCCGCTAAATTTTGTATTTTCATTAGA 1089
QY 359 GlyGlyValSerProTyrLeuSerGlyTyrSerGlnTrpProAspLeuArg 375
Db 1090 GCGGGGTTTACCATTATTTGTCAGGCTGTCTCAAACTCTGACCTCAGG 1140

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RESULT 15

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US-09-964-667-4
; Sequence 4, Application US/09964667
; Publication No. US20030033621A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,667
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-964-667-4
Alignment Scores:
Pred. No.: 1,08e-171 Length: 1418
Score: 1787.00 Matches: 363
Percent Similarity: 95.54% Conservatives: 1
Best Local Similarity: 95.28% Mismatches: 11
Query Match: 87.86% Indels: 10
DB: 10 Gaps: 0
US-09-380-203-2 (1-375) x US-09-964-667-4 (1-1418)
QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 14 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 73
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProVal-AlaGlyIle 40
Db 74 AACCTCCGCTCCCGGGTTTCAAGCGATTCTCTGCTCAGCCTCCCGCAGTAGCTGGAT 133
QY 40 eThrGlyMetCysThrHisAlaArgLeuLeuLeuPhePheLeuValGluMetGluPh 60
Db 134 TACAGCATGTGCAC-CACGCTCGGCTAATTTTGTATTTTGTAGTAGAGATGAGTT 192
QY 60 eLeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerValSerAl 80
Db 193 TCTCCATGTTGTGTCAGGCTGGTCTCGAACT-CGACCTCAGATGATCTCCGCTCTCGGC 251
QY 80 aSerGlnSerAlaArgTyrArgThrGlyHisAlaArg-LeuCysLeuAlaAsnPheC 100
Db 252 CTCCTCAAAAGTGTAGATACAGGACTGAGCACCATTGCGGCTCTGCTGGCTAAATTTT 311
QY 100 ySGlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerT 120
Db 312 GTGGTAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGCTCAAGCAGTCCA 371
QY 120 hrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheI 140
Db 372 CTGCTCTCAGCTCCCAAAGTCTGGATTACAGGCGTGACGCGTGGCTGGCTTTTAA 431
QY 140 leLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
Db 432 TTTTATTTTTTAAAGACACAGGCTGCCACTCTTACCAGGATGAAGTGCAGTGGTGTG 491
QY 160 spHisSerSerLeuGlnProSerThrProGluIleIysHisProProAlaSerAlaSerG 180
Db 492 ATCAGAGCTCACTGACGCTTCAACTCT-GAGATCAAGCATCTCTCTGCTCAGCCTCCC 550
QY 180 In-ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePhe 199
Db 551 AAGTAGCTGGACCAAGACATGCACCACTACACTGCTGCTAATTTTATTTTATTTT 610
QY 200 AsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
Db 611 AATTTTTTGGAGACAGAGTCTCAACTCTGTCCAGGCTGGAGTGCAGTGGCGCAATCTT 670
QY 220 GlySerLeuGlnProLeuProGlyPheLeuPheSerCysProSerLeuLeuSer 239
Db 671 GGCTCACTGCAACTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCGCACTCTCGAGT 730
QY 240 SerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMet 259
Db 731 AGCTGGAGCTACAGGCGCCACACCGCTAGCTAAATTTTGTATTTTAGTAGAGATG 790
QY 260 -GlyPheThrMetPheAlaArgLeuLeuLeu-ileSerGlyProCysAspLeuProAlas 279
Db 791 GGGTTTTCACCATGTTCCGCGGTTGATGCTAGATCTCTTGACCTTGTGATCTGCTGCT 850

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Db |||||
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Db |||||
QY 299 PheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsn 318
Db |||||
QY 911 TTTTGTGTTTGGAAATGGAATCTCACTCTGTTACCCAGGCTGGAGTGCAATGGCCAAAT 970
Db |||||
QY 319 LeuGlySerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuPro 338
Db |||||
QY 971 CTCGGCTCACTGCAACCTCTGCCTCCCGGCTCAAGCGATTCTCCTGTCTCAGCCTCCCA 1030
Db |||||
QY 339 SerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArg 358
Db |||||
QY 1031 AGCAGCTGGGATTACGGGCACCTGCA-CCACACCCCGCTAAATTTTGTATTTTCATTAGA 1089
Db |||||
QY 359 GlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db |||||
QY 1090 GGCGGGGTTTACCATTATTTGTGAGGCTGGTCTCAAACTCTGACCTCAGG 1140
Db |||||

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Job time : 828 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2005, 22:21:14 ; Search time 222 Seconds
(without alignments)
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	2034	100.0 1442	2 US-08-454-557C-120 Sequence 120, App
2	2034	100.0 1442	2 US-08-340-426D-120 Sequence 120, App
3	2034	100.0 1442	2 US-08-450-673C-120 Sequence 120, App
4	2034	100.0 1442	2 US-09-872-968-1 Sequence 1, Appl
5	1787	87.9 1418	5 PCT-US95-1711A-120 Sequence 120, App
6	1520	74.7 1381	2 US-08-454-557C-49 Sequence 49, Appl
7	1520	74.7 1381	2 US-08-340-426D-49 Sequence 49, Appl
8	1520	74.7 1381	2 US-08-450-673C-49 Sequence 49, Appl
9	1520	74.7 1381	5 PCT-US95-1711A-49 Sequence 49, Appl
10	913	44.9 9779	4 US-09-949-016-15370 Sequence 15370, A
11	908	44.6 107980	4 US-09-949-016-14370 Sequence 14370, A
12	885	43.5 50518	4 US-09-949-016-12315 Sequence 12315, A

ALIGNMENTS

RESULT 1

US-08-454-557C-120

; Sequence 120, Application US/08454557C

; Patent No. 5830670

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection of Alzheimer's Disease

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/454,557C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; REFERENCE/DOCKET NUMBER: 0609.3840003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 120:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1442 base pairs

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Sequence 12462, A
Sequence 17085, A
Sequence 12175, A
Sequence 12511, A
Sequence 13725, A
Sequence 13064, A
Sequence 12715, A
Sequence 14045, A
Sequence 12608, A
Sequence 16287, A
Sequence 14786, A
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Sequence 13627, A
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Sequence 15797, A

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
US-08-454-557C-120

Alignment Scores:
Pred. No.: 3 52e-184 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-380-203-2 (1-375) x US-08-454-557C-120 (1-1442)

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QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGGCTCCCGGGTTCAAGCGATTCTCTGCGCTCAGCCTCCCGAGTAGCTGGATT 134
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QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
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QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCTCAGGCTCCCAAGTGTGGGATTACAGCGTGCAGCGCTGCTGGCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTTTTAAGACACAGGTGTCCCACTCTTACCAGGATGAAGTGCAGTGGTGTAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTCAGCGCTTCAACTCTCGAGATCAAGCATCTCTGCTCCCTCAGCCTCCCAA 554
QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCATCACCTGAGTCAAGCATCTCTGCTCCCTCAGCCTCCCAA 554
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
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QY 241 TrpAspTyrArgArgProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGGCGCCACACGCCCTAGCTAATTTTTTGTATTTTTTAGTAGAGATGGGG 794
QY 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
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Db 1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTCAGGCTGGTCTCAAACTCTCTGACCTCAGG 1139

RESULT 2
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; Sequence 120, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
US-08-340-426D-120

Alignment Scores:
Pred. No.: 3 52e-184 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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; Sequence 120, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..1139
US-08-450-673C-120
Alignment Scores:
Pred. No.: 3.52e-184 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
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Db 435 TTATTTTATTTTAAAGACACAGGTGTCCCACTCTTACCAGATGAAGTGCAGTGGTGTAT 494

QY 161 HisSerSerLeuGlnProSerThrProGluLeuLysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTCAGCGCTTCAACTCTCTGAGATCAAGCATCTCTCTGCTCAGCCTCCCA 554

QY 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuLysPhePheLePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCACTACACCTGCTGCTAAATTTTATTTTATTTTAA 614

QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
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QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
Db 675 TCACGTGAACCTCTGCCTCCCGGTTCAAGTTATTTCTCTGCTGCCAGCTCTCTGAGTAGC 734

QY 241 TrpAspTyrArgProProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGGCCACACAGCGCTAGCTAAATTTTGTATTTTATTTAGTAGAGTGGG 794

QY 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280
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RESULT 4

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US-09-872-968-1
; Sequence 1, Application US/09872968
; Patent No. 6770797
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration

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; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/09/872,968
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-968-1

Alignment Scores:
Pred. No.: 3,52e-184 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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US-09-380-203-2 (1-375) x US-09-872-968-1 (1-1442)

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QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCGCTCGGCC 254

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QY 261 PheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAla 280
 Db 795 TTCACCATGTTGCCAGGTTGATCTTGACCTCTGGACCTTGTCATCTGCTGCTCGGC 854
 QY 281 SerGlnSerAlaGlyLeuThrGlyValSerHisHisAlaArgLeuLeuPheAsnPheCys 300
 Db 855 TCCCAAAGTCTGGGATTACAGCGGTGAGCCACCGCCGGCTTATTTTAAATTTTGT 914
 QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
 Db 915 TTGTTTGAATGGAATCTCACTCTGTACCCAGCTGGAGTGCATGGCCAAATCTCGGC 974
 QY 321 SerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
 Db 975 TCACGTCAACCTCTGCTCCCGGCTCAAGCGATTCTCTGTCTCAGCCTCCCAACGAGC 1034
 QY 341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysLeuPheLeuArgGlyGly 360
 Db 1035 TGGGATTACGGGACCTGCGCCACACACCGCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
 QY 361 ValSerProTyrLeuSerGlyTyrSerGlnThrProAspLeuArg 375
 Db 1095 GTTTCACCATATTGTGAGGCTGGTCTCAAACTCTTGACCTCAGG 1139

RESULT 5

PCT-US95-17111A-120
 ; Sequence 120. Application PC/TUS951711A
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
 ; TITLE OF INVENTION: Detection of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/17111A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/340,426
 ; FILING DATE: 14-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609.3840002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 120:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1418 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; NAME/KEY: CDS
 ; LOCATION: 14..1418
 PCT-US95-17111A-120

Alignment Scores:
 Pred. No.: 1.2e-160 Length: 1418
 Score: 1787.00 Matches: 363

Percent Similarity: 95.54% Conservative: 1
 Best Local Similarity: 95.28% Mismatches: 11
 Query Match: 87.86% Indels: 10
 DB: 5 Gaps: 0
 US-09-380-203-2 (1-375) x PCT-US95-17111A-120 (1-1418)
 QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
 Db 14 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 73
 QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProVal-AlaGlyIle 40
 Db 74 AACCTCCGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCGCAGTAGGCTGGAT 133
 QY 40 eThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetCluPh 60
 Db 134 TACAGCATGTGCAC-CACGCTCGGCTAATTTTGTATTTTTTTTAGTAGAGATGGAGTT 192
 QY 60 eLeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAl 80
 Db 193 TCTCCATGTTGTCAGGCTGGTCTCGAACT-CGACCTCAGATGATCTCTCCGCTCTCGGC 251
 QY 80 aSerGlnSerAlaArgTyrArgThrGlyHisAlaArg-LeuCysLeuAlaAsnPheC 100
 Db 252 CTCCCAAGTGTAGATACAGACTGAGCACCATGCGCGCTCTGCTGGCTAAATTTT 311
 QY 100 YsGlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerT 120
 Db 312 GTGGTAGAAACAGGGTTTCACTGATGTGCCAAGTGGTCTCTGAGCTCAAGCAGTCCA 371
 QY 120 hrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheI 140
 Db 372 CTGCTCAGCTCCCAAGTGTGGATTACAGGCTGACGCCGTGCTGCTGGCTTTT 431
 QY 140 leLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
 Db 432 TTTTATTTTTTAAAGACACAGGTGTCCCACTTTACCAGGATGAAGTGAGTGGTG 491
 QY 160 sPHisSerSerLeuGlnProSerThrProGluLeuLysHisProProAlaSerAlaSerG 180
 Db 492 ATCAGAGCTCACTGAGGCTTCAACTCT-GAGATCAAGCATCTCTCTGCTCAGCCTCCC 550
 QY 180 In-ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuLeuPheIlePheLePhe 199
 Db 551 AAAGTAGCTGGGACCAAGACATGACCACTACACTGCTAAATTTTATTTTATTTT 610
 QY 200 AsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
 Db 611 AATTTTTTGGAGACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGCAGTGGCGCAATCT 670
 QY 220 GlySerLeuGlnProLeuProProGlyPheLysLeuPheSerCysProSerLeuLeuSer 239
 Db 671 GGCTCACTGCAACCTCTGCTCCCGGTTCAAGATTATTCTCTGCCCGCAGCTCTCGAGT 730
 QY 240 SerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMet 259
 Db 731 AGCTGGACTACAGGCGGCCACCAAGCTAGCTAATTTTGTATTTTATTTAGTAGAGATG 790
 QY 260 -GlyPheThrMetPheAlaArgLeuLeuLeu-IleSerGlyProCysAspLeuProAlaAs 279
 Db 791 GGGTTTCAACATGTTCCGCGAGGTTGATGTAGATCTCTGACCTGTGTGATCTGCTGCTC 850
 QY 279 erAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis-AlaArgLeuLeuPheAsn 298
 Db 851 CGGCTCCCAAGTCTGGGATTACAGGACGTGAGCGCCACCGCCGCGCTATTTTAAAT 910
 QY 299 PheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsn 318
 Db 911 TTTTGTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCATGGCCAAAT 970
 QY 319 LeuGlySerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuPro 338

Db 971 CTCGGCTCACTGCAACCTCTGCTCCCGGGCTCAAGCAGATTCTCCTGTCTCAGCCTCCCA 1030
 Qy 339 SerSerTrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheLeArg 358
 Db 1031 AGCAGCTGGGATTACGGGACCTGCA-CCACACCCCGCTAAATTTTGTATTTTCATTAGA 1089
 Qy 359 GlyGlyValSerProTyrLeuSerGlyTyrSerGlnThrProAspLeuArg 375
 Db 1090 GCGGGGTTTACCATATTGTGAGGCTGGTCTCAAACTCTCGACCTCAGG 1140

RESULT 6

US-08-454-557C-49
 ; Sequence 49, Application US/08454557C
 ; Patent No. 5830670
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wanda, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; TITLE OF INVENTION: of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,557C
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609.3840003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1381 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; US-08-454-557C-49

Alignment Scores:
 Pred. No.: 3,25e-135 Length: 1381
 Score: 1520.00 Matches: 344
 Percent Similarity: 90.16% Conservative: 4
 Best Local Similarity: 89.13% Mismatches: 25
 Query Match: 74.73% Indels: 22
 DB: 2 Gaps: 3

US-09-380-203-2 (1-375) x US-08-454-557C-49 (1-1381)
 Qy 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
 Db 14 ATGGAGTTTTCGCTCTGTGTCCCGAGGCTGGAGTGAATGGCGCAATCTCAGCTCAGCGC 73
 Qy 21 AnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
 Db 74 AACCTCCGCTCCCGGTTCAAGCATCTCTGTGCTCAGCTCCCGAGTAGCTGGGATT 133
 Qy 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
 Db 134 ACAGCAGTGTGCAC-CACGCTCGGCTAAATTTTGTATTTTGTATTTTGTAGTAGAGTAGGATT 192

Qy 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerA 80
 Db 193 AACTCCATGTTGGTCAGGCTGCTCGAACTCCCGACCTCAGATGATCTCCGCTCGCGC 252
 Qy 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
 Db 253 CTGCCCAAGTGTCTGAGATT---ACAGGATGAGCCACCATGCGCGGCTCTGCTGGCT 309
 Qy 98 AnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeu 117
 Db 310 AATTTTGTGTAGAAACAGGGTTTCACTGATGTTGTCACCAAGTGTCTCTGAGCTCAA 369
 Qy 117 sGlnSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProG 137
 Db 370 GAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGGCTCA-GCGTGCCTGG 428
 Qy 137 YLeuPheIleLeuPheLeuArgHisArgCysProThrLeuThrGlnAspGluValG 157
 Db 429 CTTTATTTATTTATTTTATTTTAAAGACACAGGTGTACCACTCTTACCCAGGATGAAGTGA 488
 Qy 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuLys-HisProAla 177
 Db 489 GTGGTGTGATCACAGCTCACTGAGCTTCAACTCTCAGATCAAGCAATCTCTGCT 548
 Qy 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePhe 197
 Db 549 CAGCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGTA-ATTTTATTT 607
 Qy 197 heIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTPA 217
 Db 608 TTAATTTTAAATTTTGTAGACAGAGTCTCAC-TCTGTCAACCCAGGCTGGAGTGCAGTGC 666
 Qy 217 rGAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
 Db 667 GCAATCTTGGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTTCTCTGCCCCAGCC 726
 Qy 237 euLeuSerSerTrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuV 257
 Db 727 TCCTGAGTAGCTGGGACTACAGGCGCCACCACGCTAGCTAAATTTTGTATTTTAG 786
 Qy 257 alGluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeu 276
 Db 787 TAGAGATGGGTTTCAACATGTTCCGCAAGTTGATCTTGATCTCTTGACCTTGTGATCTG 846
 Qy 277 ProAlaSerAla-SerGlnSerAlaGlyIleThrGly-ValSerHisHisAlaArgLeu 296
 Db 847 CTGCTCGGCTACCCAAAGTGTGGGATTACAGGTCTGACTCCACGC---CGGCCTA 903
 Qy 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnT 316
 Db 904 TTTTAAATTTTGTGTTGTAATGGAATCTCACTCTGTACCAGGTCGAGAGTCAAT 963
 Qy 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeu 336
 Db 964 GGCA-AATCTCGGCTACTCGCAACCTCTGCTCCCGGTC-AAGCGATTCTCTGTCTCA 1021
 Qy 336 erLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIleP 356
 Db 1022 GCCTCCCAAGCAGCTGGGATTACGGAC-CTGCA-CCACACCCGCTAAATTTTGTATTT 1079
 Qy 356 heIleArgGlyGlyValSerProTyrLeuSerGlyTyrP-SerGlnThrProAspLeuArg 375
 Db 1080 TCATTAGAGCGGGTTTA--CCATATTGTGAGGCTGGGTCTCAAACTCTCGACCTCAGG 1137

RESULT 7

US-08-340-426D-49
 ; Sequence 49, Application US/08340426D
 ; Patent No. 5948634
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wanda, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.,
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/340,426D
 FILING DATE: 14-NOV-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0609,3840002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1381 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both

US-08-340-426D-49

Alignment Scores:
 Pred. No.: 3,25e-135 Length: 1381
 Score: 1520.00 Matches: 344
 Percent Similarity: 90.16% Conservative: 4
 Best Local Similarity: 89.12% Mismatches: 25
 Query Match: 74.73% Indels: 22
 DB: 2 Gaps: 3

US-09-380-203-2 (1-375) x US-08-340-426D-49 (1-1381)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaSerAlaHisArg 20
 Db 14 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGAATGGCGCAATCTCAGCTACCGC 73
 QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyLe 40
 Db 74 AACCTCCGCTCCCGGGTTCAGCGGATCTCTGCTCCAGCTCCCGCTCCCGCTGGGATT 133
 QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrrPhePheLeuValGluMetGluPhe 60
 Db 134 ACAGGATGTGAC-CACGCTCGGCTAAATTTGTATTTTTTTTAGTAGAGATGGAGTTT 192
 QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerA 80
 Db 193 AACTCCATGTGGTCAGGCTGGTCTGAACTCCGACCTCAGATGATCTCCGCTCCGCG 252
 QY 80 laSerGlnSerAlaArgTyrrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
 Db 253 CTGCCAAAGTGTGAGATT--ACAGGATGAGCCACCATGCCGCGCTCTGCTGGGT 309
 QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeu 117
 Db 310 AATTTTTGGTAGAACAAGGGTTTCACTGATGTGGCCCAAGCTGGTCTCTGAGCTCAA 369
 QY 117 sGlnSerThrCysLeuSerLeuProLysCysTrpAspTyrrArgAlaAlaValProGln 137
 Db 370 GCAGTCACCTGCCTCAGCTCCCAAGTGTGGGATTACAGCGCTCA-GCCGTGCTGG 428
 QY 137 YLeuPheLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGln 157
 Db 429 CCTTTTATTTATTTTATTTTAAAGACACAGGTGTACCACTCTTACCAGGATGAAGTGCA 488

QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuLeuHisProProAla 177
 Db 489 GTGGTGTGATCACAGCTACTGAGCTTTCAACTCTGAGATCAAGCAATCTCTCTGCCT 548
 QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrrThrTrpLeuLeuPheIleP 197
 Db 549 CAGCCTCCCAAGTAGCTGGGACCAAGACATGACCACTACACCTGGTA-ATTTTATTT 607
 QY 197 heilePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
 Db 608 TTATTTTAAATTTTGTGACAGAGTCTCAC-TCTGTCAACCAAGCTGGAGTGGAGTGGC 666
 QY 217 iqAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
 Db 667 GCAATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCGCC 726
 QY 237 euLeuSerSerTrpAspTyrrArgArgProProArgLeuAlaAsnPhePheValPheLeu 257
 Db 727 TCCTGAGTAGCTGGGACTACAGCGCCACCACTAGCTAATTTTGTATTTTAG 786
 QY 257 alGluMet-GlyPheThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeu 276
 Db 787 TAGAGATGGGGTTTCAACATGTTCCAGGTTGATCTTGTATCTTGTGATCTG 846
 QY 277 ProAlaSerAla-SerGlnSerAlaGlyLeuThrGly-ValSerHisHisAlaArgLeu 296
 Db 847 CTGCTCGGCTCACTCCCAAGTCTGGGATTACAGGTCGTGACTCCACGC---CGGCCTA 903
 QY 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGln 316
 Db 904 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTACCACGGTGGAGTGCAAT 963
 QY 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeu 336
 Db 964 GGCA-AATCTCGGCTACTCGCAACCTCTGCTCCCGGGTC-AAGCGATTCTCTGTCTCA 1021
 QY 336 erLeuProSerSerTrpAspTyrrGlyHisLeuProProHisProAlaAsnPheCysIleP 356
 Db 1022 GCCTCCCAAGCAGCTGGGATTACGGGAC-CTGCA-CCACACCCCGCTAATTTTGTATT 1079
 QY 356 heileArgGlyGlyValSerProTyrrLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
 Db 1080 TCATTAGAGCGGGTTTA--CCATATTGTGAGGCTGGTCTCAAACTCTCAGCTCAG 1137

RESULT 8

US-08-450-673C-49
 Sequence 49, Application US/08450673C
 Patent No. 5948888

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
 TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 TITLE OF INVENTION: of Alzheimer's Disease
 NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,673C
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.

```

; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-450-673C-49

Alignment Scores:
Pred. No.: 3,25e-135 Length: 1381
Score: 1520.00 Matches: 344
Percent Similarity: 90.16% Conservativity: 4
Best Local Similarity: 89.12% Mismatches: 25
Query Match: 74.73% Indels: 22
DB: 3 Gaps: 3

US-09-380-203-2 (1-375) x US-08-450-673C-49 (1-1381)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 14 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACGCC 73

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
DB 74 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCCGCAGTAGCTGGATT 133

QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
DB 134 ACAGGCAATGTGCAC-CACGCTCGGCTAAATTTTGTATTTTATTTTATAGATGGAGTTT 192

QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerA 80
DB 193 AACTCCATGTTGTGAGGCTGGTCTCGAACTCCGACCTCAGATGATCTCCGCTCGGC 252

QY 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
DB 253 CTGCCCAAAGTGTGAGATT---ACAGGCATGAGCCACCATGCCCGGCTCTGCTGGCT 309

QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuIly 117
DB 310 AATTTTGTGTAGAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTCTCTGAGCTCAA 369

QY 117 sGlnSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGl 137
DB 370 GCAGTCCACTGCTGCTCAGCTCCCAAAGTGGGATACAGCGGTCA-GCCGTGCTGG 428

QY 137 YLeuPheIleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGl 157
DB 429 CCTTTTATTTTATTTTATTTTAAAGACACAGGTGTACCACTCTTACCAGGATGAAGTGCA 488

QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluIleLys-HisProProAlaS 177
DB 489 GTGGTGTGATCAGCTCAGCTCAGCTCCAAAGTGGGATACAGCGGTCA-GCCGTGCTGG 548

QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisIstYrThrTrpLeuIlePheIleP 197
DB 549 CAGCTTCCCAAGTAGCTGGGACCAAGATGACCATGACCATCTACCTGGTA-ATTTTATTT 607

QY 197 heilePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
DB 608 TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 666

QY 217 rgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
DB 667 GCAATCTGGCTCAGCTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTCCCGCCAGCC 726

QY 237 euLeuSerSerTrpAspTyrArgArgProProArgLeuAlaAsnPheValPheLeuV 257

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DB 727 TCCTGAGTAGCTGGGACTACAGGGCCCAACAGCGCTAGCTAAATTTTTTGTATTTTAG 786
QY 257 alGluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeu 276
DB 787 TAGAGATGGGGTTTCACCATGTTGCCAGGTTGATCTTGTGATCTCTTGACCTTGTGATCTG 846
QY 277 ProAlaSerAla-SerGlnSerAlaGlyIleThrGly-ValSerHisAlaArgLeuI 296
DB 847 CCTGCTCGGCTACCCAAAGTGTGGGATTTACAGTCTGACTCCACGC---CGGCCTA 903
QY 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnT 316
DB 904 TTTTAAATTTTGTGTTTGAATGGATCTCACTCTGTACCAGGTCGAGTGCAAT 963
QY 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuS 336
DB 964 GGCA-AATCTCGGCTACTCGCAACCTCTGCCTCCCGGTC-AAGCGATTCTCTCTCTCA 1021
QY 336 erLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIleP 356
DB 1022 GCCTCCCAAGCAGCTGGGATTTACGGGAC-CTGCA-CCACACCCCTAATTTTGTATTT 1079
QY 356 heileArgGlyGlyValSerProTyrLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
DB 1080 TCATTAGAGCGGGTTTA--CCATATTTGTAGGCTGGTCTCAAACTCTTGACCTCAGG 1137

RESULT 9
PCT-US95-17111A-49
; Sequence 49, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
PCT-US95-17111A-49

Alignment Scores:
Pred. No.: 3,25e-135 Length: 1381
Score: 1520.00 Matches: 344
Percent Similarity: 90.16% Conservativity: 4

```

Best Local Similarity: 89.12% Mismatches: 25
Query Match: 74.73% Indels: 22
DB: 5 Gaps: 3

US-09-380-203-2 (1-375) x PCT-US95-17111A-49 (1-1381)

```
QY 1 MetGluPheSerLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
Db 14 ATGGAGTTTTCGCTCTGTGGCCAGGCTGGAGTCAATGGCGCAATCTCAGCTCACCG 73
QY 21 AnnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 74 AACCTCCGCTCCCGGGTTCAGCGGATTCCTCGCTCAGCTCCCGCTCCCGTAGCTGGATT 133
QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyPhePheLeuValGluMetGluPhe 60
Db 134 ACAGGATGTGCAC-CACGCTGGCTAAATTTGTATTTTGTATTTTGTAGATGAGATT 192
QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspSerProValSerA 80
Db 193 AACTTCATGTGTGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCTCCGCTCGGC 252
QY 80 laSerGlnSerAlaArgTyArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
Db 253 CTGCCCAAGTGTGAGATT---ACAGGCATGAGCCACCATGCCCGGCTCTGCCTGGCT 309
QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuIy 117
Db 310 AATTTTGTGTAGAAACAGGGTTTCACGTATGTGCCCAAGCTGTCTCTCGAGCTCA 369
QY 117 sGlnSerThrCysLeuSerLeuProLysCysTrpAspTyArgArgAlaAlaValProGl 137
Db 370 CGAGTCCACCTCGCTCAGCCTCCCAAAGTGTGGGATTACAGCGGTCA-GCCGTGCTGG 428
QY 137 yLeuPheLeuLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGl 157
Db 429 CCTTTTATTTTATTTTATTTTATTTTAAAGACACAGGTGTACCACTCTTACCAGGATGA 488
QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuLys-HisProAlaAs 177
Db 489 GTGGTGTGATCAAGCTCACTGACGCTTCAACTCTGAGATCAAGCAATCTCTCTGCT 548
QY 177 exAlaSerGlnValAlaGlyThrLysAspMetHisHisTyThrTrpLeuIlePheIleP 197
Db 549 CAGCCTCCCAAGTAGTGGGACCAAGACATGACCACTACACCTGTTA-ATTTTATTT 607
QY 197 heIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
Db 608 TTATTTTAAATTTTGTGAGACAGAGTCTCAC-TCTGTCAACCCAGGCTGGAGTGCAGTGC 666
QY 217 tGAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
Db 667 GCAATCTTGCTCACTGCAACCTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCGCAGCC 726
QY 237 euLeuSerSerTrpAspTyArgArgProProArgLeuAlaAsnPhePheValPheLeuV 257
Db 727 TCCTGAGTAGCTGGGACTACAGCGGCCCAACCGCTAGCTAGTAATTTTGTATTTTAG 786
QY 257 alGluMet-GlyPheThrMetPheAlaArgLeuLeuLeuIleSerGlyProCysAspLeu 276
Db 787 TAGAGATGGGGTTTCAACATGTTTCGCCAGGTTGATCTTGTACCTTGTGATCTG 846
QY 277 ProAlaSerAla-SerGlnSerAlaGlyIleThrGly-ValSerHisHisAlaArgLeuI 296
Db 847 CTGCTCGCTCGCTTACCAAGGTGCGGATTACAGGTGTGACTCCAGCC---CGGCCTA 903
QY 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnT 316
Db 904 TTTTAAATTTTGTGTTGAAATGGAATCTCACTCTGTTACCGAGGTGGAGTGCAAT 963
QY 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuS 336
Db 964 GCACA-AATCTCGGCTACTCGCAACCTCTGCTCCCGGGTCA-AAGCGATTCTCTCTCTCA 1021
```

```
QY 336 erLeuProSerSerTrpAspTyArgGlyHisLeuProProHisProAlaAsnPheCysIleP 356
Db 1022 GCCTCCCAAGCAGCTGGGATTACGGGAC-CTGCA-CCACACCCCGCTAAATTTTGTATT 1079
QY 356 heIleArgGlyGlyValSerProTyArgLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
Db 1080 TCATTAGAGCGGGTTTA--CCATATTCTCAGGCTGGGTCTCAAACTCTGACCTCAGG 1137
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RESULT 10

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US-09-949-016-15370
; Sequence 15370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO011307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15370
; LENGTH: 9779
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15370
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Alignment Scores:

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Pred. No.: 4,428-76 Length: 9779
Score: 913.00 Matches: 239
Percent Similarity: 59.76% Conservative: 15
Best Local Similarity: 56.24% Mismatches: 112
Query Match: 44.89% Indels: 62
DB: 4 Gaps: 10
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US-09-380-203-2 (1-375) x US-09-949-016-15370 (1-9779)

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QY 4 SerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgHisLeuArg 23
Db 3685 TCACCTTTGTGGCCAGGCTGGAGTGCATGTGCAATCTCGGCTCACCGCAATCTCCGC 3744
QY 24 LeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMet 43
Db 3745 CTCCTGGGTTCAACAATTTCTCTCGCTCAGCCTCCGAGTAGCTGGGATTATAGGCATA 3804
QY 44 CysThrHisAlaArgLeuLeuLeuTyPhePheLeuValGluMetGluPheLeuHisVal 63
Db 3805 CGCCACCATGCTGCTGCTAATTTGTAT---TTTAA-GTAGAGACGGGGTTTCTCCATGTT 3860
QY 64 GlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAlaSerGlnSer 83
Db 3861 GGTCAAGCTGATCTTGAACCTCCCAACCTCAGCTGATCCACCTGCTGCCCTCCCAAGT 3920
QY 84 AlaArgTyArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAsn 103
Db 3921 GCTGGAATTACAGCATGAGCCACTGCG-----GCCTGGCCTAATTTTGTATTTTAAAT 3974
QY 104 ArgValSerLeuMetCysProSer---TrpSer-----ProGluLeuLysGlnSerThr 120
Db 3975 AGGGTT---TTGTATGTTGGTCACTGCTGCTCAAAACCTCCACATCAACTGATCTGCC 4031
QY 121 CysLeuSerLeuProLysCysTyPheAspTyArgArgAlaAlaValProGly-----Leu 138
Db 4032 TGCCTCAGCCTTCAAAAGTGTGGGATTACAGGGGTGA-GCCATGCGCACATAACTTCCTT 4090
QY 139 PheIleLeuPhePheLeuArgHisArgCysPro---ThrLeu-ThrGlnAspGluValGl 157
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QY 176 AlaSerAlaSerGlnValAlaGlyThrLysAspMetHisHisThrTrpLeuIlePhe 195
Db 22741 GCTTAGCCTCTGAGTAGCTGGATTACAGGCACGCCACCACCGCCAGGCTAATTTT 22682
QY 196 IlePheIle----- 198
Db 22681 GTATTTTGTAGTAGACAGCGGGTTTCCACCATTTTGGCCAGGCTGGTCTTGAATTCCTGACT 22622
QY 198 ----- 198
Db 22621 TCGTGATCGCCTGCTCAGCCTCCCAAGAGTCTGGGATTACAGCGGTGAGCCACACAC 22562
QY 199 -----PheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGln 215
Db 22561 CTGGCCTATTATTTTGTAGATGGAGTCTTGC-TCTGTTGCCAGGCTGAGTGCAG 22503
QY 216 TrpArgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysPro 235
Db 22502 TGGTGCCATCTTGGCTCACTGCAACCTCGCCTCTGGGTTTCAAGTGAATTCCTCGCCTC 22443
QY 236 SerLeuLeuSerSerTrpAspTyrArgArg---ProProArgLeuAlaAsn----- 251
Db 22442 ACGTCCCGAGTAGCTGGATTACAGCGCCCAAGCCACCATGCGCGCTAATTTTGTATT 22383
QY 252 ----PhePheValPheLeuValGluMetGlyPheThrMetPheAla---ArgLeu----- 267
Db 22382 TCTTTTTTTTTTTTTTTTGTAGATGGAGTCTCACTTGTGCGCCAGGCTGAGTGC 22323
QY 268 -----IleLeuIleSerGlyProCysAspLeuProAla 278
Db 22322 AACAGTGGCATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGCGATTCTCTGCC 22263
QY 279 SerAlaSerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePhe-As 298
Db 22262 TCAGCTCCGAGTAGCTGGGATTACAGCGCAAGCCACCATGCGCGCTAATTTTGTGA 22203
QY 298 nPheCysLeu-----PheGluMetGluSerHisSer-ValThrGlnAlaGlyValG 315
Db 22202 TTTCTTTCTTTTTTTTTTTTGTAGATGGAGTCTCACTTGTCACTAGGCTGAGTGC 22143
QY 315 InTrpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysL 335
Db 22142 AACGGTGGCATCTTGGCTCACTGCAACCTCTGCTCCCGGGTTCAAGCGATTCTCTGCC 22083
QY 335 euSerLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysI 355
Db 22082 TCAGCTCTTGTAGTACCTGGGATTATAGATGCTGCTGCCACCATGCGCGCTAATTTTGTGA 22023
QY 355 IlePheIleArgGlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuA 375
Db 22022 TTTGTAGTAGACAGCGGTTTCCACCATATTGAACAGGCTGGTCTCGAACTCTTGACCTCA 21963
QY 375 rg 375
Db 21962 GG 21961

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RESULT 12
US-09-949-016-12315/c
; Sequence 12315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

```

```

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12315
; LENGTH: 50518
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12315

Alignment Scores:
Pred. No.: 2,41e-72 Length: 50518
Score: 885.00 Matches: 236
Percent Similarity: 51.86% Conservative: 29
Best Local Similarity: 46.18% Mismatches: 101
Query Match: 43.51% Indels: 147
DB: 4 Gaps: 12

US-09-380-203-2 (1-375) x US-09-949-016-12315 (1-50518)
QY 4 SerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArg 23
Db 39610 TCACCTTGTGGCCAGGCTGAGTGCATGGCGTGGTCTCGGCTCATGGCAACATCTGC 39551
QY 24 LeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMet 43
Db 39550 CTCCCGGTTTCAAGCCATTCTCTGCTCAACCTCCCAAGTAGCTGGGATTACAGGTGTG 39491
QY 44 CysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPheLeuHisVal 63
Db 39490 CGCCACTATGCCAGCTAATTTTATATATTTTGTAGAGATGAGGTTCACCATGTT 39434
QY 64 GlyGlnAlaGlyLeuGluLeuProThrSerAspSerProSerValSerAlaSerGlnSer 83
Db 39433 GGCCAGGCTTGTGCAAACTCTGACCTGAGGTGATCCACCCACTCAGCCTCCCAAGT 39374
QY 84 AlaArgTyrArgThr---GlyHisHisAlaArg-Leu----- 94
Db 39373 GCTGGGATTACAAGCATGAGCCACCGCGCGCTATATTTATTTATTTTATTTTATTT 39314
QY 94 ----- 94
Db 39313 ACTTATTTATTTGACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 39254
QY 94 ----- 94
Db 39253 GTCTTGTCTCTCACCCAGGCTGAAGTGCATGCAATGGCATGCTCTGCTCACTGCAACCC 39194
QY 94 ----- 94
Db 39193 ACTTCCAGGTTCAAGCAATTTCTCTGCTCAGCCTCCCGAGTAGCTGGGACTACAGGTG 39134
QY 95 -----CysLeuAlaAsnPheCys-----GlyArgAsnArgValSerLeuMetCys 109
Db 39133 TGTGCCACCATGCTGGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT 39082
QY 109 sProSerTrp-----SerProGluLeuLysGlnSerThrCysLeuSerIle 124
Db 39081 -CCATATGGCCAGGCTAATCTCGAATCTCTGAGCTCAGGTGATCGCCCTCGGCT 39023
QY 124 uProLysCysTrpAspTyrArgArgAlaAlaVal---ProGlyLeuPheIleLeuPhePhe 143
Db 39022 CCCAAATGCTGAGATTACAGCGGTGAGCCACACACCGCTCTTTTGT---TTTT 38966
QY 143 eLeu-ArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAspHisSerS 163
Db 38965 TTTGAGATGGGATCTCACTCTTTCACCCAGCCAGATGAGTGGGAGAAATCATAGCT 38906
QY 163 erLeuGlnProSerThrProGluIleLys-HisProProAlaSerAlaSerGlnValAla 182
Db 38905 CACTGCAGCATCGAACTCTCTGAGCTCAAGGATCTCTCCAGCTCAGCCACCTAGTAGCT 38846
QY 183 GlyThrLysAspMetHisHisThrTrpLeuIlePheIlePheLeuPheAsnPheLeu 202
Db 38845 GGGATCAAAAGGTGTGCACCATGCTAATTTGTGTAA-TTTTTTTTTTTTTTTT 38787

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QY 203 ArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeu 222
Db 38786 AGATGGAGTCTT---GCTGTACCCAGCGCTGGAGTGCAGTGGTGCATCTCAGCTCACTG 38730
QY 223 GlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAsp 242
Db 38729 CAACCTCTGCCCTCCAGGGTTCAAGCAGTTCTCTGCCTCAGCCTCTTGTAGTAGTAGGAC 38670
QY 243 TyrArg---ArgProProArgLeuAlaAsnPheValPheLeuValGluMetGlyPhe 261
Db 38669 TACAAGTGCCCAACCCACACCTGGCTAATTTTGTATTTTAGTAG-AGACAGGGTTTC 38611
QY 262 ThrMetPheAlaArgLeuLeuLeuSerGlyProCysAspLeuProAlaSerAlaSer 281
Db 38610 ACCATGTTGGTCTGAGGTGCTCGAACTCTCGAACCTCTGTGATCTGCGCTCCTCAGCCTCC 38551
QY 282 GlnSerAlaGlyLeuThrGlyValSerHisAlaA--- 293
Db 38550 CAAAGTCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCTGTTTAAATTTTTTAGAGA 38491
QY 294 -----ArgLeuIlePheAsn----- 298
Db 38490 CGGGGTCTTGCTATGTGGCCAGGCTGGTCTCGAACTCTCGCCTCAGGCAATCCTTCCA 38431
QY 298 ----- 298
Db 38430 CCTCAGCTATCTGAGAGTACTGGGATTATAGGAAGAGCCATGGCACCCTGGTGGCTT 38371
QY 299 -----PheCysLeuPheGluMetGluSer 306
Db 38370 GTTACATTTTAAATCCCTATTGCTCTCTACTCTTTTCTTTTCTTTTTCGAGACAGTCT 38311
QY 307 HisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGlnProLeuPro 326
Db 38310 TGCCTCGTCCCCAGCGCTGGAGTACAGTGGTGGATCTCAGCTCACTGCAACCTCCGCT 38251
QY 327 ProGlyLeuLysArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeu 346
Db 38250 CTGGGTTCACGGGTCTCTCGCCTCAGCCTCCGAGTAGTAGAATTTACAGACATTTCA 38191
QY 347 ProProHisProAlaAsnPheCysIlePheIleArgGlyGlyValSerProTyrLeuSer 366
Db 38190 ACACATGCCAGCTAATTTTGTATTTTAGTAGAGACAGGGTTTCGCCATGTTAGCCA 38131
QY 367 GlyTrpSerGlnThrProAspLeuArg 375
Db 38130 GACTAGTCTCAAACTCCTGACCTCAGG 38104
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RESULT 13

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US-09-949-016-13718
; Sequence 13718, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13718
; LENGTH: 14411
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13718
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Alignment Scores:
Pred. No.: 7,13e-72 Length: 14411
Score: 871.50 Matches: 250
Percent Similarity: 45.62% Conservative: 21
Best Local Similarity: 42.09% Mismatches: 99
Query Match: 42.85% Indels: 231
DB: 4 Gaps: 9

US-09-380-203-2 (1-375) x US-09-949-016-13718 (1-14411)
QY 1 MetGluPheSerLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db 5680 ATGGAGTTTG-CTCTGTGCCAGGTGGAGTGCATTTGGCTCACTGC 5738
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 5739 AACCTCCGCTCCAGGTTCAAGCAATTTCTCTGCTCAGTCCCCCAAGTAGCTGGATT 5798
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuPhePheLeuValGluMetGluPhe 60
Db 5799 ACAGCAGCTGCGCACACACAGCTAATTT--TTTGTATTTTATAGTAGACGGGTTT 5856
QY 61 LeuHisValGlyGlnAlaGlyLeuCluLeuProThrSerAspSerProSerValSerAla 80
Db 5857 CTCCATGTGTGTCAGGTGGTCTCAACTCTCAGCTCAGGTGATCCACCGCCTCGGCC 5916
QY 81 SerGlnSerAla-----ArgTyrArgThr----- 88
Db 5917 TCCCAAAATGTGGGATTACAGGATGAGCCACCGCGCTGGCCTCCCACCTCTTTAT 5976
QY 88 ----- 88
Db 5977 GTCCTGTCTGGAACACAGCAGCCCCGCTCTCCCGAGTAGAGAAGTGACGCCACTAATCGG 6036
QY 89 GlyHisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAsnArgVal---SerLeu 107
Db 6037 GGTATACATCTTTGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 6096
QY 108 MetCysProSerTrpSer----- 113
Db 6097 CGTTGCCAGGCTGGAGTGCAATGTCAGATCTCGGCTCAGTGCACCACTCTTCTCGCTGC 6156
QY 113 ----- 113
Db 6157 TGGGTTCAAGCAATTTCTCTGTCTCAGCCTCAGTAGTAGTGGGATTACAGSCACCGCC 6216
QY 113 ----- 113
Db 6217 ACCATGCCAGCTAATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTT 6276
QY 114 -----ProGluLeuLysGlnSerThrCysLeuSerLeuPro 125
Db 6277 TGTGTATCAGGCTGATCTTTGAACCTCTGACCTCAGGTGATCCACCCACCTCAGCCTCCA 6336
QY 126 LysCysTrpAspTyrArgArg--AlaAlaValProGlyLeu----- 138
Db 6337 AAGTCTGGAATTACAGGCGTGAGCCACTGTGCCGCGCTCACATCTTTTGTATTTTATACCA 6396
QY 138 ----- 138
Db 6397 CCAATGTTTATTTTATTTTATTTATATATATATATATATATATATATATATATATATAT 6456
QY 138 ----- 138
Db 6457 TGTTCCTTGTGCCCAAGTTGGAGTGCATGGCACGATCTCAGCTCATTGCAACCTCTGC 6516
QY 138 ----- 138
Db 6517 CTCCGGGTTCAAGTGATTCTCTCGCCTCAGCCTCCTGAGTAGTGGGAAATACAGCGCT 6576
QY 139 -----PheIleLeuPhePheLeuArgHisArgCysProThrL 151
Db 139 -----PheIleLeuPhePheLeuArgHisArgCysProThrL 151
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Db 6577 CGCACACACACCCAGCTAAATTTTTTTTTTTTTTTTTTTTTTTTGGAGACGAGTCTCGCTTT-G 6635
Qy 151 euThrGlnAapGluValGlnTrpCysAspHisSerSerLeuGlnProSerThrProGluI 171
Db 6636 TCGCCAGGTGGAGTGCAGTGGTGAATCTGACTCACTGCAACTTCGGCTCCAGCT 6695
Qy 171 lelyHisProProAlaSerAlaSerGlnValAlaGlyThrlysAspMetHisHisTyr 191
Db 6696 TCAAGCACTTCTCTGCTCAGCTCGCGAGTAGCTGGATTACAGTCCGCTGCCACCATG 6755
Qy 191 hrTrpLeullePhelePhe----- 197
Db 6756 CTGGCTAAATTTTTTT-TTTTTGATATTTTGTAGTACAGAGGGTTTTTACCATCTGGCCA 6814
Qy 197 ----- 197
Db 6815 GGCTGCTCTTAACCTCTGACCTCGTGATCCACCCCTCAGCTCCCAAGTGTGAGA 6874
Qy 198 -----IlePheAsnPheLeuArgGlnSerLeuA 207
Db 6875 TTACAGGTGTAGCCACCATGCTCGCCAAATTTTATTTATTTTATTTGAGACAGAGTCTCG 6934
Qy 207 snSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGlnProLeuProp 227
Db 6935 C-TCTGTGCCAGGTGGAGTGCAGTGTGATACAACTTGCTCACTGCAACCTCGCCCTC 6993
Qy 227 roGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAspTyrArgAtg---P 246
Db 6994 CCGGGTTTAAAGCAATTTCTCTGCTCAGCTTCCTGAGTAGCTGGAGTCAAGCGCGTGC 7053
Qy 246 roProArgLeuAlaAsnPhePheValPheLeuValGluMetGly-PheThrMetPheAla 265
Db 7054 CACCATGCCCGGCTAA-TTTTTTGTGTTTTTAGTAGACAGAGATTTTACCATTGTGGCC 7112
Qy 266 ArgLeulleLeulleSerGlyProCysAspLeuProAlaSerAlaSerGlnSerAlaGly 285
Db 7113 AGCGTGTCTCGATCTCTGACCTCATGATCTGCTGCTCGCTCGCCCTCCCAAGTGTGAG 7172
Qy 286 IleThrGlyValSerHisHisAlaArgLeuLeullePheAsn-----PheCysLeuPheGlu 303
Db 7173 ATTACAGGTGGAGCCAGCTGCTGCGCAATTTTTTGTG-TATTTTTTTTTTTTTTTTGGAG 7231
Qy 304 MetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGln 323
Db 7232 ATGGAGTCTCGCTCTCTGCGCCAGGTGGAGTGCAGTGCAGTGCAGTGCCTCCCTGCAA 7291
Qy 324 ProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuProSerSerTrpAspTyr 343
Db 7292 GCTCCGCTCTCTGGGTTCACACCATTTCTCTGCTCAGCTCCCGAGTAGCTGGGACTAC 7351
Qy 344 GlyHisLeuProProHisProAlaAsn-PheCysIlePheIleArgGlyGlyValSerPr 363
Db 7352 AGGTGCCCGCCAGCGCCAGCTAAATTTTTGTATTTTATTTAGTAGAGATGGGGTTTACC 7411
Qy 363 ofYrLeuSerGlyTrpSerGlnTrpProAspLeu 374
Db 7412 G-----TGCTCTCTATCTCTCGACCTC 7433
RESULT 14
US-09-949-016-12462/c
; Sequence 12462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

```
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12462
; LENGTH: 56616
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(56616)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12462

Alignment Scores:
Pred. No.: 1,07e-70 Length: 56616
Score: 868.50 Matches: 231
Percent Similarity: 57.04% Conservative: 16
Best Local Similarity: 53.35% Mismatches: 94
Query Match: 42.70% Indels: 96
DB: 4 Gaps: 12

US-09-380-203-2 (1-375) x US-09-949-016-12462 (1-56616)
Qy 5 LeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeu 24
Db 45864 CTCCTTTGTTGCCAGACTGGAGTGCACCGCGTGATCTCAGCTCATTTGCCAACCTCTGCTTC 45805
Qy 25 ProGlySerSerAspSerProAlaSerAlaSerProAlaGlyIleThrGlyMetCys 44
Db 45804 CCAGGTTTCAAGTGATTTCTCTGACTCAGCTCCCAAGTAGCTGGGATTAAGGCGGCACAC 45745
Qy 45 ThrHisAlaArgLeuLeulleLeuTyrPhePheLeuValGluMetGlyPheLeuHisValGly 64
Db 45744 CACCACACCCACTA-----TTTTTAGTAGAGATGGGTTTTCACGCTGTGTGT 45697
Qy 65 GlnAlaGlyLeuGluLeuProThrSerAspProSerValSerAlaSerGlnSerAla 84
Db 45696 CAGGCTGGTCTGAACTCTGACTCAGCTCAGCTGATCGCTCGCTCCCTCCCAAGTGTCT 45637
Qy 85 ArgTyrArgThrGly-----HisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArg 102
Db 45636 GGGATT---ACAGGATGAGCCACCCAGCC----- 45610
Qy 103 AsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeu 122
Db 45609 -----TGG-----CCCCAGTAGAAGCGCTACGTGTACT 45580
Qy 123 -----SerLeuProLysCysTrpAspTyrArg----- 132
Db 45579 CCCCATTTCATCAATAAGGATATTACAAAGAGTTGCAATTTTACAGACTAATAATTTTAC 45520
Qy 133 -----AlaAlaValProGlyLeuPheIleLeuPhePheLeuArgHisArgCysPro 149
Db 45519 CACCTCATCAAGGCCATTCTCT-----TTTTTTTTTTTGTAGATG-GAGTATCAC 45473
Qy 150 ThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeuGlnProSerThrPro 169
Db 45472 TCTGTCAACCCAGGTGGAGTGCAGTGGTGCAGTCTCGGCTCACTGCAAACTCTGCCCTCCC 45413
Qy 170 GluIle-LysHisProProAlaSerAlaSerGlnValAlaGlyThrLysAspMetHisHi 189
Db 45412 AGTTTCACGCCATTCTCTGCTCAGCCCCCGAGTAGCTGGAGTACAGGTGCCACCA 45353
Qy 189 sTyrThrTrpLeullePheIlePheAsn----- 200
Db 45352 CCACGCCCGGCTAAATTTTTTGT-----ATTTTAGTAGAGACGAGGGTTTTCACCATGTAGCC 45296
Qy 200 ----- 200
Db 45295 AGGATGGTCTCGATCTCTGACCTCATGATCTGCTGCTGCTGCTGCTGCCAAGTGTAGG 45236
Qy 201 -----PheLeuArgGlnSerLeuAsnSerVa 209
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Db 45235 ATGACAGGCATGAGCCACCGTGCCCGAGCCTTTTCTTTTGTAGATGAAGTCTCGCTTGT 45176
Qy 209 lThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGlnProLeuProGlyPh 229
Db 45175 CGCCAGGCTGGAGTACAATGGCACAATCTCGGCTCACTGCAATCTCCGCTCTGGGT 45116
Qy 229 eLysLeuPheSerCysProSerLeuLeuSerSerTrpAspTyrArgPro---ProAr 248
Db 45115 CRAAGCAATTCTCTGCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACCCACTAGCAG 45056
Qy 248 gLeuAlaAsnPhePheValPheLeuValGluMet-GlyPheThrMetPheAlaArgLeuI 268
Db 45055 CCAGCTAATT---TTTGTATTTTAGATAGATGGGTTTACCATGTGGCCAGGCTGG 44998
Qy 268 leLeuIleSerGlyPro--CysAspLeuProAlaSerAlaSerGlnSerAlaGlyIleTh 287
Db 44997 TCTCGAACTCTGACCTCAGCGCATCTGCCACCTCGGCTCCCAAAGTACTGAGATTAC 44938
Qy 287 rGlyValSerHisHisAlaArgLeuIle-----PheAsnPheCysLeuPheGluMetGl 305
Db 44937 AGCGCTGAGCCACTGCGCCTC-ACCATCAAGGCCATTCTTTTGTGTTT-TTTGAGATGGA 44880
Qy 305 uSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGlnProLe 325
Db 44879 GTCTCACTCTGTGGCCAGCTGGAGTGAGTGGCAGATCTTGGCTCACTGCAACCTCT 44820
Qy 325 uProGlyLeuLysArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHi 345
Db 44819 GCCTCTGGGTTCAAGTGATTTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCA 44760
Qy 345 sLeuProProHisProAlaAsnPheCysIlePheIleArgGlyValSerProTyrIle 365
Db 44759 CCTGCCACCACATCCAGCTGCTTTTGTGTTTGTAGATAGATGGGTTTCCCATGTTG 44700
Qy 365 uSerGlyTyrSerGlnThrProAspLeuArg 375
Db 44699 ACCAGATGCTCGAACTCTCGACCGCAGG 44669

RESULT 15
US-09-949-016-17085/c
; Sequence 17085, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17085
; LENGTH: 56616
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(56616)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17085
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Alignment Scores:
Pred. No.: 1.07e-70 Length: 56616
Score: 868.50 Matches: 231
Percent Similarity: 57.04% Conservative: 16
Best Local Similarity: 53.35% Mismatches: 94

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Query Match: 42.70% Indels: 96
DB: 4 Gaps: 12
US-09-380-203-2 (1-375) x US-09-949-016-17085 (1-56616)
Qy 5 LeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeu 24
Db 45864 CTCCTGTTGCCAGACTGAGTGCACCGCGTGATCTCAGCTCATTGCAACCTCTGCTTC 45805
Qy 25 ProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCys 44
Db 45804 CCAGGTTCAAGTGATCTCTCCTGACTCAGCTCCCAAGTAGCTGGGATTAAAGCGCACAC 45745
Qy 45 ThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPheLeuHisValGly 64
Db 45744 CACCACACCCAGCTA-----TTTTTAGTAGATGGGTTTTCACCTGCGTTGCT 45697
Qy 65 GlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAlaSerGlnSerAla 84
Db 45696 CAGGCTGGTCTCGAACTCTGACCTCAGGTGATCCGCTCGCTTGGCTTCCCAAAGTGTCT 45637
Qy 85 ArgTyrArgThrGly-----HisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArg 102
Db 45636 GGGATT---ACAGGCATGAGCCACCCAGCC----- 45610
Qy 103 AnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeu 122
Db 45609 -----TCG---CCCCAGTAAAGAGCGCTACGTGTACT 45580
Qy 123 -----SerLeuProLysCysTrpAspTyrArgArg----- 132
Db 45579 CCCCATTTCATCAATAAGGATATTACAAGAGTTCCAAATTACAGACTAATAATTTTATC 45520
Qy 133 -----AlaAlaValProGlyLeuPheIleLeuPheLeuArgHisArgCysPro 149
Db 45519 CACCTCATCAAGGCCATTCT-----TTTTTTTTTTCAGATG-GAGTATCAC 45473
Qy 150 ThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeuGlnProSerThrPro 169
Db 45472 TCTGTCAACCCAGGCTGGAGTGCGAGTGGCGCATCTCGGCTCACTCCAACTCTGCTCCC 45413
Qy 170 GluIle-LysHisProProAlaSerAlaSerGlnValAlaGlyThrLysAspMetHisHi 189
Db 45412 AGGTTACGCCCATTTCTTCTGCTCAGCCCCCGAGTAGCTGGGACTACAGGTGCCACCA 45353
Qy 189 sTyrThrTrpLeuIlePheIlePheAsn----- 200
Db 45352 CCACCCCGGCTAATTTTTTGT---ATTTTAGTAGACAGCGGGTTTCACCATGTAGCC 45296
Qy 200 ----- 200
Db 45295 AGGATGGTCTCGATCTCTGACCTCATGATCTGCTGCTCGACTCCCAAGTCTAGG 45236
Qy 201 -----PheLeuArgGlnSerLeuAsnSerVa 209
Db 45235 ATGACAGGCATGAGCCACCGTGCCCGAGCCTTTTCTTTTGTAGATGAAGTCTCGCTTGT 45176
Qy 209 lThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGlnProLeuProGlyPh 229
Db 45175 CGCCCGAGGCTGGAGTACAATGGCACAATCTCGGCTCACTGCAATCTCCGCTCTCTGGGTT 45116
Qy 229 eLysLeuPheSerCysProSerSerLeuLeuSerSerTrpAspTyrArgArgPro---ProAr 248
Db 45115 CAAGCAATTCTCTGCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACCCACTAGCAGC 45056
Qy 248 gLeuAlaAsnPhePheValPheLeuValGluMet-GlyPheThrMetPheAlaArgLeuI 268
Db 45055 CCAGCTAATT---TTTGTATTTTAGTAGATGGGTTTACCATGTGGCCAGGCTGG 44998
Qy 268 leLeuIleSerGlyPro--CysAspLeuProAlaSerAlaSerGlnSerAlaGlyIleTh 287
Db 44997 TCTCGAACTCTCTGACCTCAGCGCATCTGCCACCTCGGCTCCCAAAGTACTGAGATTAC 44938
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QY 305 uSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGlnProLe 325
Db 44879 GTCTCACTCTGTGTGCCAGGCTGGAGTGCAGTGGCAGAATCTTGGCTCACTGCAACCTCT 44820
QY 325 uProProGlyLeuLeuArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHi 345
Db 44819 GCCTCTGGGTTCAAGTGATTTTCCTGCTTCAGCCTCCCGAGTAGCTGGGATTTACAGGCA 44760
QY 345 sLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGlyValSerProTyrLe 365
Db 44759 CCTGCCACCACATCCAGCTGCTTTTGTGTTTGTAGTAGAGATGGGGTTTCACCATGTTG 44700
QY 365 uSerGlyTrpSerGlnThrProAspLeuArg 375
Db 44699 ACCAGGATGCTCTCGAACTCTGACCGCAGG 44669
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Search completed: September 16, 2005, 01:30:19
Job time : 325 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2005, 18:46:18 ; Search time 670 seconds
(without alignments)
3313.288 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MFESLLPRLECNCAISAH.....FIRGGVSPYLQSGWSTPDLR 375

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q/cn2_1/USFTO.spool/US09380203/runat_13092005_170810_11663/app_query.fasta_1.519
-DB=N Geneseq 16Dec04 -OFT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US09380203@CN_1.1.644 @runat_13092005_170810_11663 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	100.0	1442	6	ABN89470
2	2034	100.0	1442	6	ABD46671
3	2034	100.0	1442	8	ABX08221
4	2034	100.0	1442	8	ABZ23236
5	2034	100.0	1442	8	AAL54224

6	2034	100.0	1442	10	ADB37519	Human neu
7	2034	100.0	1442	10	ACC84453	AD7C-NTP
8	2034	100.0	1442	13	ADR14408	Human NF-
9	1787	87.9	1418	2	AAT27738	Neural th
10	1517	74.6	1381	2	AAQ77883	Neural th
11	1517	74.6	1381	2	AAT27765	AD 10-7 h
12	964.5	47.4	75252	11	ACN44450	Human gen
13	901	44.3	33362	13	ABD32700	Human can
14	892.5	43.9	92638	6	ABO88096	Human ost
15	885	43.5	173805	10	ADL13775	Osteoarth
16	869.5	42.7	24345	13	ADS36503	Human aut
17	869.5	42.7	40947	13	ADS36474	Human aut
18	863.5	42.5	110096	6	ABN95044	Gene #154
19	861.5	42.4	21666	9	ADA02702	Human Nup
20	861.5	42.4	21666	10	ADB72440	Human CA
21	861.5	42.4	21666	10	ADE95950	Human hCG
22	858	42.2	126001	12	ADH77123	Human PAZ
23	857.5	42.2	24167	5	ABA16132	Human ner
24	857.5	42.2	59999	13	ADR28249	Human low
25	857	42.1	32865	11	ACN44490	Human gen
26	852	41.9	167932	10	ADL13501	Osteoarth
27	851.5	41.9	3379	10	ADH63278	Human ocp
28	851.5	41.9	3379	12	ADF91770	Human G-p
29	848.5	41.7	15783	4	AAK90159	Human dig
30	848.5	41.7	15783	5	AAK90159	Genomic s
31	848.5	41.7	15783	9	ADB32763	Human nov
32	848	41.7	61103	11	ACN43886	Human gen
33	846	41.6	124987	12	ADP03055	Human hou
34	846	41.6	124990	13	ADS88553	Human hou
35	842.5	41.4	173805	10	ADL13775	Osteoarth
36	841.5	41.4	40645	8	ABX61804	Genomic D
37	841.5	41.4	40645	9	ADA49717	Genomic D
38	841	41.3	190117	10	ADL13780	Osteoarth
39	840.5	41.3	50000	10	ADC58843	Human IKB
40	840	41.3	27148	4	AAS28612	Genomic s
41	840	41.3	27148	10	ADG41808	Human res
42	840	41.3	27148	11	ADI97582	Human res
43	840	41.3	74234	11	ACN44594	Human gen
44	840	41.3	79544	12	ADQ97764	Human can
45	839	41.2	73063	12	ADQ97727	Human can

ALIGNMENTS

RESULT 1
ABN89470
ID ABN89470 standard; DNA; 1442 BP.

XX AC ABN89470;

XX DT 02-SEP-2002 (first entry)

XX DE Neural thread protein (NTP) encoding nucleotide sequence.

XX KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
XX KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
XX KW hypoxia; ischaemia; cerebral infarction; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 15..1142
XX FT /*tag= a
XX FT /product= "Neural thread protein"

XX PN WO200234915-A2.

XX PD 02-MAY-2002.

XX PF 25-OCT-2001; 2001WO-US042813.

XX PR 27-OCT-2000; 2000US-00697590.

KW cosmetic modification; vascular disease; atherosclerosis;
KW arterioclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease; gene; ds.
XX Homo sapiens.
XX OS
XX WO200297030-A2.
XX PN
XX PD
XX 05-DEC-2002.
XX PF
XX 24-MAY-2002; 2002WO-COA000759.
XX PR
XX 25-MAY-2001; 2001US-0293156P.
XX (NYMO-) NYMOX CORP.
XX PA
XX Averbach PA;
XX PI
XX WPI; 2003-041406/03.
XX DR
XX Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX PT
XX PS
XX Disclosure; Fig 1; 78pp; English.
XX CC
XX The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
CC disease. This sequence encodes the human neural thread protein AD7C-NTP
XX
XX SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,7e-149 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-380-203-2 (1-375) x ABX08221 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
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Db 15 ATGGAGTTTTCGCTCTTGTGTTGCCAGGCTGGAGTCAATGGCGCAATCTCAGCTCACCGC 74
QY 21 AenLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
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QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGATGTGACCCACGCTCGGCTAATTTTGTATTTTATTTTATTTAGTAGAGTAGAGTTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCCGCTCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAGTGTAGATACAGGACTGGCCACCATGCTCCGCTCTGCTGGCTAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
Db 315 GGTGAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTCGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyrrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCTCCCAAGTGTCTGGGATTACAGGCGTGCAGCGTGCCTGGCCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTGCAGTGGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGCAGCCTTCAACTCTGAGATCAAGCATCTCTCTGCTCAGCCTCCCAA 554
QY 181 ValAlaGlyThrLysAspMetHisIstYrrTrpLeuIlePheIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCCTACCTGGCTAATTTTATTTTATTTTAAAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTCAACCCAGGCTGGAGTGCAGTGGCGCAATCTTGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerSerLeuSerSer 240
Db 675 TCATCTGCAACCTCTCTCCCTCCCGGGTTCAAGTTATTTCTCTGCCCCAGCCTCTCTGAGTAGC 734
QY 241 TrpAspTyrrArgArgProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGCGCCACCCAGCTAGCTAATTTTGTATTTTGTATTTAGTAGAGTGGGG 794
QY 261 PheThrMetPheAlaArgLeuIleLeuSerGlyProCysAspLeuProAlaSerAla 280
Db 795 TTCACTCATGTTTCCGCGAGTTGATCTGTGACCTTGTGATCTGCTCCCTCGCTCGGCC 854
QY 281 SerGlnSerAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePheAsnPheCys 300
Db 855 TCCCAAAGTGTGGGATTACAGGCGTGAACACACCGCCGCTTATTTTATTTTGT 914
QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGAATGGCAATCTCGGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCATCTGCAACCTCTCTCCCGGGTCAAGCGAATTTCTCTGTCTCAGCTCCCAAGCAGC 1034
QY 341 TrpAspTyrrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGGCACCTGCCACACACCCCGCTAATTTTGTATTTTCAATTAGAGCGGG 1094
QY 361 ValSerProTyrrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTGAGGCTGGTCTCAAACTCTCAACCTCCTGACCTCAGG 1139

RESULT 4

ABZ23236
 ID ABZ23236 standard; DNA; 1442 BP.
 XX
 AC ABZ23236;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Nucleotide sequence of human neuronal thread protein AD7c-NTP.
 XX
 KW Human; neuronal thread protein; AD7c-NTP; Alzheimer's disease; histone;
 KW neurodegeneration; in vivo gene expression; amphipathic compound;
 KW gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 CDS 15..1142

FT /*tag= a

FT /product= "neuronal thread protein AD7c-NTP"

XX WO200299036-A2.

XX 12-DEC-2002.

XX 28-MAY-2002; 2002WO-US016429.

XX 01-JUN-2001; 2001US-00872968.

XX (RHOD-) RHODE ISLAND HOSPITAL.

XX Wanda JR, De La Monte SM;

XX WPI; 2003-140605/13.

XX P-PSDB; ABB99774.

XX Inducing prolonged in vivo gene expression in mammal by contacting
 PT neuronal tissue with composition comprising Alzheimer's disease-
 PT associated neural thread protein 7c antisense nucleic acid, histone,
 PT amphipathic compound.

XX Disclosure; Page 34-35; 69pp; English.

XX The present sequence encodes a human neuronal thread protein AD7c-NTP.
 CC AD7c-NTP is overexpressed in brains with Alzheimer's disease at early and
 CC intermediate stages of neurodegeneration. The expression of AD7c-NTP may
 CC be reduced using the method of the invention. The specification describes
 CC a method for inducing prolonged in vivo gene expression in a mammal. The
 CC method comprises contacting a non-muscular tissue with a composition
 CC comprising a nucleic acid, histone and an amphipathic compound. The
 CC method is useful for inducing prolonged in vivo gene expression in non-
 CC muscular tissue of a mammal, e.g. neuronal tissue, central nervous system
 CC (CNS) tissue, tissue comprising a post-mitotic neuronal cell, cortical
 CC neuronal cell or hippocampal neuronal cell, glial cell, or vascular
 CC endothelial cell. The method is useful in gene therapy applications to
 CC treat Alzheimer's disease, where the composition comprises antisense
 CC AD7c-NTP nucleic acid

XX SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,7e-149 Length: 1442
 Score: 2034.00 Matches: 375
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-380-203-2 (1-375) x ABZ23236 (1-1442)

Qy 1 MetGluPheSerLeuLeuProGluGluCysAsnGlyValAlaIleSerAlaHisArg 20

Db 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCATATGGCGCAATCTCAGCTCACCGC 74
 Qy 21 AenLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValIleGlyIle 40
 Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTCGCTCAGCCTCCCGCTAGCTGGGATT 134
 Qy 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
 Db 135 ACAGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTATTTTATTTAGTAGAGATGGAGTTT 194
 Qy 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
 Db 195 CTCATATTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCCGCTCTCGGC 254
 Qy 81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
 Db 255 TCCCAAGTGTAGATACAGGACTGGCCACCATGCCGCTCTGCTGGCTAATTTTGT 314
 Qy 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
 Db 315 GGTAGAACACAGGTTTCACTGATGTGCCNAGCTGCTCTCTGAGCTCAAGCAGTCCACC 374
 Qy 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
 Db 375 TGCCTCAGCTCCCAAGTGTGGATTACAGCGCTGACGCGTGCCTGGCCTTTTATT 434
 Qy 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
 Db 435 TTAATTTTTTAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTGCAGTGGTGTGAT 494
 Qy 161 HisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerGln 180
 Db 495 CACAGCTCACTGCAGCTTCAACTCTGAGATCAGCATCTCTCTGCTCAGCTCCCAA 554
 Qy 181 ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheIlePheAsn 200
 Db 555 GTAGTGGGACCAAGACATGCACCATACACCTGCTAAATTTTATTTTATTTTAAAT 614
 Qy 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
 Db 615 TTTTGGACAGAGTCTCACTCTGTCCACGAGTGGAGTGCAGTGGCGCAATCTTGGC 674
 Qy 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
 Db 675 TCACCTGCAACTCTGCTCCCGGGTTCAAGTTATTTCTCTGCCCCAGGCTCTCTGAGTAGC 734
 Qy 241 TrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
 Db 735 TGGGACTACAGGCGCCACCAACGCTAGCTAATTTTGTATTTTATTTAGTAGAGATGGGG 794
 Qy 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
 Db 795 TTCACCATGTTCGCGAGGTGATCTTGATCTCTGGACCTTGATCTGCTGCTGCTGCTGCGC 854
 Qy 281 SerGlnSerAlaGlyIleThrGlyValSerHisAlaArgLeuIlePheAsnPheCys 300
 Db 855 TCCCAAGTGTGGGATTACAGGCTGAGCCACACGCGCCGCTTATTTTAAATTTTGT 914
 Qy 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
 Db 915 TTGTTGAAATGGAATCTCACTCTGTACCAGGCTGGAGTGCATATGGCAATCTCGGC 974
 Qy 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
 Db 975 TCACCTGCAACTCTGCTCCCGGGCTCAAGCGATTCTCTGCTCAGGCTCTCCAGAGCAGC 1034
 Qy 341 TrpAspTyrGlyHisLeuProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
 Db 1035 TGGGATTACGGGACCTGCCACACACCCCGCTAATTTTGTATTTTATTTAGTAGAGCGGG 1094
 Qy 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
 Db 1095 GTTTTCAACCATATTGTGAGGCTGGTCTCAAACTCTCTGACCTCAGG 1139

Db 1035 TGGGATTACGGGACCTGCACACACCCCGCTAAATTTTGTATTTTCAATTAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTTCAGGCTGGTCTCAAACTCCTGACCTCAGG 1139

RESULT 7
ACC84453
ID ACC84453 standard; DNA; 1442 BP.
XX ACC84453;
AC ACC84453;
XX 28-AUG-2003 (first entry)
XX AD7c-NTP encoding sequence.
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX Unidentified.
XX WO2003008443-A2.
XX 30-JAN-2003.
XX 19-JUL-2002; 2002WO-CA001105.
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX (NYMO-) NYMOX CORP.
XX Averbach PA;
XX WPI; 2003-2479999/24.
XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX Disclosure; Fig 1; 77pp; English.

CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
XX
SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.7e-149 Length: 1442
Score: 2034.00 Matches: 375
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-380-203-2 (1-375) x ACC84453 (1-1442)
QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyValAlaIleSerAlaHisArg 20
Db 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACCGC 74

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db 75 AACCTCCGCCCTCCCGGGTTCAAGCGATTCTCTGCTCAGCGCTCCCGAGTAGCTGGATT 134
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
Db 135 ACAGGCATGTGCACCCACGCTCGGCTAAATTTTGTATTTTATTTAGTAGAGATGGAGTTT 194
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
Db 195 CTCCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCGCTCGGCC 254
QY 81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
Db 255 TCCCAAAAGTGTAGATACAGGACTGGCCACCATGCGCGCTCTGCTGCTGCTAAATTTTGT 314
QY 101 GlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThr 120
Db 315 GGTAGAAAACAGGGTTTCACTGATGTGCCCAAGCTGGTCTCTCTGAGCTCAAGCAGTCCACC 374
QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
Db 375 TGCCTCAGCCTCCCAAGTGTGGGATTACAGGCGTGCAGCGCTGCTGGCCTTTTATT 434
QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
Db 435 TTATTTTTTTTAAAGACACAGGTGTCCCACTCTTACCCAGGATGAAGTGCAGTGTGTGAT 494
QY 161 HisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerGln 180
Db 495 CACAGCTCACTGCGAGCCTTCAACTCCTGAGATCAAGCATCTCTCTGCTGCTCAGCCTCCCAA 554
QY 181 ValAlaGlyThrLysAspMetHisTyrThrTrpLeuIlePheIlePheAsn 200
Db 555 GTAGCTGGGACCAAGACATGCACCCTACCTGCTAAATTTTATTTTATTTTAAAT 614
QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
Db 615 TTTTGTAGACAGAGTCTCAACTCTGTCAACCAGGCTGGAGTGCAGTGGCGCAATCTTGGC 674
QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSerSer 240
Db 675 TCACGTCAACCTCTGCTCCTCCCGGTTCAAGTTATTTCTCTGCCCCAGCCTCTCTGAGTAGC 734
QY 241 TrpAspTyrArgArgProArgLeuAlaAsnPheValPheLeuValGluMetGly 260
Db 735 TGGGACTACAGCGCGCCACCCAGCTAGCTAAATTTTGTATTTTATTTAGTAGAGATGGG 794
QY 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280
Db 795 TTCACCATGTTGGCCAGGTTGATCTTGATCTCTGGACCTTGTGATCTGCTGCTCGCC 854
QY 281 SerGlnSerAlaGlyIleThrGlyValSerHisAlaArgLeuIlePheAsnPheCys 300
Db 855 TCCCAAAAGTGTGGGATTACAGCGGTGAGCACACCGCCGCTTATTTTAAATTTTGT 914
QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
Db 915 TTGTTTGAATGGAATCTCACTCTGTATCCAGGCTGGAGTGCATGGCAATGCGCAATCTCGC 974
QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
Db 975 TCACGTGCAACCTCTGCTCCTCCCGGCTCAAGCGATTCTCTGCTCAGGCTTCCCAAGCAGC 1034
QY 341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
Db 1035 TGGGATTACGGGCACCTGCGCACCAACCCCGCTAAATTTTGTATTTTATTTATTTAGAGCGGG 1094
QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
Db 1095 GTTTCACCATATTTGTACAGGCTGGTCTCAAACTCCTGACCTCAGG 1139

RESULT 8

ADRI14408
 ID ADRI14408 standard; DNA; 1442 BP.
 XX AC ADRI14408;
 XX DT 21-OCT-2004 (first entry)
 XX DE Human NF-kappaB pathway-associated gene SeqID409.
 XX DE
 KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antarthritic; antiarthritis; gastrointestinal-Gen; antiasthmatic;
 KW antihistaminic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; gene, ds; human.
 XX Homo sapiens.
 OS
 XX
 XX WO2004065577-A2.
 XX
 XX 05-AUG-2004.
 XX
 PF 13-JAN-2004; 2004WO-US0000798.
 XX
 PR 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 PI
 XX
 XX WPI: 2004-562168/54.
 DR P-PSDB; ADRI14409.
 DR
 XX
 PT New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX
 XX Claim 1; SEQ ID NO 409; 237pp; English.
 PS
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antiarthritis,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant

CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human gene which is
 CC subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX

SQ Sequence 1442 BP; 314 A; 402 C; 311 G; 415 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.7e-149 Length: 1442
 Score: 2034.00 Matches: 375
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09:380-203-2 (1-375) x ADRI14408 (1-1442)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
 Db 15 ATGGAGTTTTCGCTCTTGTGGCCAGGCTGGAGTGCATATGGCGCAATCTCAGCTCACC 74
 QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValaGlyIle 40
 Db 75 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTCGCTCAGCCTCCCGTAGTAGTGGATT 134
 QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
 Db 135 ACAGGCATGTGCACCCAGCTCGGCTAATTTTGTATTTTTTTTATAGTAGAGTAGGATT 194
 QY 61 LeuHisValGlyGlnAlaGlyLeuLeuProThrSerAspSerProSerValSerAla 80
 Db 195 CTCCATGTTGGTCAGCTGGTCTCGAACTCCGACCTCAGATGATCCCTCCGCTCTCGGCC 254
 QY 81 SerGlnSerAlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys 100
 Db 255 TCCCAAGTGTGTAGATACAGGACTGGCCACCATGCCGCTCTGCTGGCTAATTTTGT 314
 QY 101 GlyArgAsnArgValSerLeuMetCysProSerThrSerProGluLeuLeuGlnSerThr 120
 Db 315 GGTAGAAACAGGGTTTCATCTGATGTGCCCAAGCTGCTCTCCAGCTCAAGCAGTCCACC 374
 QY 121 CysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIle 140
 Db 375 TGCCTCAGCTCCCAAGTGTGGATTTACAGCGGTGACGCGTCCCTGGCCCTTTTATT 434
 QY 141 LeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAsp 160
 Db 435 TTATTTTTTTTAAAGACACAGGTGTCCCACTCTTACCAGGATGAAGTGCAGTGGTGTAT 494
 QY 161 HisSerSerLeuGlnProSerThrProGluLeuLysHisProAlaSerAlaSerGln 180
 Db 495 CACAGCTCACTGCAGCTTCAACTCTTGAGATCAAGCATCTCTCTGCTCAGCTCAGCTCCCA 554
 QY 181 ValAlaGlyThrLysAspMetHisIleTyrThrTrpLeuIlePheIlePheIlePheIle 200
 Db 555 GTAGCTGGGACCAAGACATGCACCATCACCTGGCTAATTTTATTTTATTTTATTTTAA 614
 QY 201 PheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGly 220
 Db 615 TTTTGTAGACAGAGTCTCAACTCTGTACCAGGCTGGAGTGCATGGCGCAATCTTGGC 674
 QY 221 SerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerSerLeuSerSer 240
 Db 675 TCAGTCAACCTTGCCTCCCGGGTTCAAGTTAATTTCTCTGCTGCCAGCCTCTCTAGTAGC 734
 QY 241 TrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuValGluMetGly 260
 Db 735 TGGGACTACAGCGCGCCACCGCTAGTAAATTTTGTATTTTATTTTATTTAGTAGAGTAGG 794
 QY 261 PheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeuProAlaSerAla 280

Db 795 TTCACCATGTCGCCAGGTGATCTTGATCTCTGGACCTTGATCTGCCTCGCTCGGCC 854

QY 281 SerGlnSerAlaGlyIleThrGlyValSerHisAlaArgLeuIlePheAsnPheCys 300
 |||||
 Db 855 TCCCAAAGTGTGGGATTACAGCGGTGAGCCACCGCCGGCTTATTTTAAATTTTGT 914
 |||||

QY 301 LeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGly 320
 |||||
 Db 915 TTGTTGAATGGAATCTCACCTCTGTACCCAGGCTGGAGTGCAATGGCCAAATCTCGGC 974
 |||||

QY 321 SerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSerLeuProSerSer 340
 |||||

Db 975 TCACTGCACACCTCTGCTCCCGGCTCAAGCGATTCTCTGCTCAGCTTCCCAAGCAGC 1034
 |||||

QY 341 TrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGly 360
 |||||

Db 1035 TGGGATTACGGGCACCTGCCACACACACCCCGCTAATTTTGTATTTCATTAGAGCGGG 1094
 |||||

QY 361 ValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
 |||||

Db 1095 GTTTCACCATATTGTGAGGCTGGTCTCAAACTCTCGACCTCAGG 1139
 |||||

RESULT 9

AAT27738

ID AAT27738 standard; DNA; 1418 BP.

XX AC AAT27738;

XX DT 13-NOV-1996 (first entry)

XX DE Neural thread protein coding sequence.

XX KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;

XX KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;

XX KW binding fragment; ds.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT 14..1207

XX FT /*tag= a

XX FT /product= "Neural thread protein."

XX PN WO9615272-Al.

XX PD 23-MAY-1996.

XX PF 14-NOV-1995; 95WO-US017111.

XX PR 14-NOV-1994; 94US-00340426.

XX PA (GENO) GEN HOSPITAL CORP.

XX PI De La Monte S, Wands JR;

XX PI WPI; 1996-259865/26.

XX DR P-FSDB; AAR95913.

XX PT Detection of neural thread protein in diagnosis of Alzheimer's disease -

XX PT also NTP DNA and protein sequences used in gene and anti:sense therapy.

XX PS Claim 24; Page 168-170; 238pp; English.

XX CC A method for detecting the presence of neural thread protein (NTP) having

XX CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject

XX CC comprises (a) contacting a sample from a human subject that is suspected

XX CC of containing the NTP with at least one molecule capable of binding to

XX CC the protein; and (b) detecting any of the molecule bound to the protein.

XX CC The binding molecule is selected from an antibody free of natural

XX CC impurities, a monoclonal antibody or a binding fragment of either of

XX CC these. The method may be used for diagnosing the presence of Alzheimer's

XX CC disease, neuroectodermal tumours and a malignant astrocytoma in a human

XX CC

SQ Sequence 1418 BP; 302 A; 396 C; 315 G; 405 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 129e-129 Length: 1418
 Score: 1787.00 Matches: 363
 Percent Similarity: 95.54% Conservative: 1
 Best Local Similarity: 95.28% Mismatches: 11
 Query Match: 87.86% Indels: 10
 DB: 2 Gaps: 0

US-09-380-203-2 (1-375) x AAT27738 (1-1418)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
 |||||

Db 14 ATGGAGTTTTCGCTCTTGTGTCAGGCTGAGTGCAATGGCGCAATCTCAGCTCAGCGC 73
 |||||

QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProVal-AlaGlyIle 40
 |||||

Db 74 AACCTCCGCTCCCGGTTCAAGCGATTCTCTGCTCAGCTCCCGAGTAGGCTGGAT 133
 |||||

QY 40 eThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPh 60
 |||||

Db 134 TACAGGCATGTGCAC-CACGCTCGGCTAATTTTGTATTATTTTATTTAGTAGAGATGAGTT 192
 |||||

QY 60 eLeuHisValGlyGlnAlaGlyLeuLeuProThrSerAspAspProSerValSerAl 80
 |||||

Db 193 TCTCCATGTTGGTCAGGCTGGTCTCGAACT-CCGACCTCAGATGATCTCCCGTCTCGGC 251
 |||||

QY 80 aSerGlnSerAlaArgTyrArgThrGlyHisAlaArg-LeuCysLeuAlaAsnPheC 100
 |||||

Db 252 CTCCCAAGTGTAGATACAGACTGAGCACCATGCTCCCGGCTCTGCTGGCTAATTTT 311
 |||||

QY 100 yslGlyArgAsnArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerT 120
 |||||

Db 312 GTGTAGAAAACAGGGTTTCACTGATGTGCCAAGTGTCTCTCAGCTCAAGCAGATCCA 371
 |||||

QY 120 hrCysLeuSerLeuProLysCysTrpAspTyrArgAlaValProGlyLeuPheI 140
 |||||

Db 372 CTGTGCTCAGCCTCCCAAAGTGTGGGATTACAGCGGTGAGCGGTGCTGGCCCTTTT 431
 |||||

QY 140 leLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysA 160
 |||||

Db 432 TTTTATTTTAAAGACACAGGTGTCCACTCTTACCAGGATGAAGTCAGTGTGTG 491
 |||||

QY 160 spHisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerG 180
 |||||

Db 492 ATCAGAGCTCACTGCAGGCTTCAACTCT-GAGATCAAGCATCTCTCTGCTCAGCCTCCC 550
 |||||

QY 180 In-ValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePhe 199
 |||||

Db 551 AAAGTAGCTGGGACCAAGACATGCACCTACACCTGGCTAATTTTATTTTATTTT 610
 |||||

QY 200 AsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu 219
 |||||

Db 611 AATTTTGTGAGACAGAGTCTCAACTCTGTACCCAGGCTGGAGTGCAGTGGCGCAATCTT 670
 |||||

QY 220 GlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSer 239
 |||||

Db 671 GGCTCACTGCAACCTCTGCTCCCGGTTCAAGTTATTCTCTGCTCCCGCCAGCCTCTCGAGT 730
 |||||

QY 240 SerTrpAspTyrArgArgProArgLeuAlaAsnPhePheValPheLeuValGluMet 259
 |||||

Db 731 AGCTGGGACTACAGGCGCCACCGCTAGCTAATTTTGTATTATTTTATTTTATTTT 790
 |||||

QY 260 -GlyPheThrMetPheAlaArgLeuIleLeu-IleSerGlyProCysAspLeuProAlaAs 279
 |||||

Db 791 GGGTTTCAACATGTTTCGCGAGGTTGATGCTAGATCTCTTGACCTTGTGTGCTGCTGCT 850
 |||||

QY 279 eAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis-AlaArgLeuIlePheAsn 298
 |||||

Db 851 CGGCTCCCAAGTGTGGGATTACAGGACGTGACGCCCGCCCGGCTTATTTTAAAT 910
 |||||

QY 299 PheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsn 318
 |||||

Db 911 TTTTGTGTTTGAATGAATCTCACTCTGTTATCCAGGCTGGAGTGCATGGCCAAAT 970
 QY 319 LeuGlySerLeuGlnProLeuProProGlyLeuLysArgPheSerCysLeuSerLeuPro 338
 Db 971 CTCGGCTCACTGAACCTCTGCTCCCGGGCTCAAGCGGATTCTCTGTCTCAGCCTCCCA 1030
 QY 339 SerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePheLeuArg 358
 Db 1031 ASCAGCTGGATTACGGGCACCTGCA-CCACACCCCGCTAAATTTTGTATTTCATTAGA 1089
 QY 359 GlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
 Db 1090 GCGCGGGTTTCAACCATATTTGTACAGCTGGTCTCAAACTCTCTGACCTCAGG 1140

RESULT 10

AAQ77883

ID AAQ77883 standard; cDNA; 1381 BP.

AC AAQ77883;

XX 25-MAR-2003 (revised)

DT 06-JUL-1995 (first entry)

XX Neural thread protein AD10-7 cDNA.

XX Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;

KW malignant astrocytomas; glioblastomas; ss.

XX Rattus rattus.

XX WO9423756-A1.

XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US004321.

XX 20-APR-1993; 93US-00050559.

XX (GEHO) GEN HOSPITAL CORP.

XX De La Monte SM, Wands JR;

XX WPI; 1994-341497/42.

XX Detection of neural thread proteins - to detect sporadic and familial

XX Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and

XX glioblastomas (Eng).

XX Example 4; Fig 16R; 158pp; English.

XX AAQ77883 is the AD10-7 neural thread protein (NTP) cDNA. This sequence

XX was used in the development of an antibody dependent method, for the

XX detection of NTPs. This new method could be used to diagnose Alzheimer's

XX disease (differentiating between sporadic and familial), neuroectodermal

XX tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-

XX 2003 to correct PN field.)

XX SQ Sequence 1381 BP; 296 A; 385 C; 301 G; 399 T; 0 U; 0 Other;

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QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
 Db 74 AACCTCCGCCCTCCCGGGTTCAAGGATTCTCTGCTCAGCTCAGCTCCCGAGTAGCTGGATT 133
 QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
 Db 134 ACAGGCATGTGCAC-CACGCTCGGCTAATTTTGTATTATTTTATTTAGTAGAGATGGAGTTT 192
 QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerA 80
 Db 193 AACTCCATGTTGGTCAGGCTGCTCGAACTCCCGACCTCAGATGATCTCCGCTCGCGC 252
 QY 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
 Db 253 CTGCCCAAGTGTCTGAGATT---ACAGGATGAGGCACCATGCCCCGGCTCTGCTGGCT 309
 QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeu 117
 Db 310 AATTTTGTGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTCTCCTCAGCTCAA 369
 QY 117 sGlnSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArgAlaAlaValProG 137
 Db 370 GCAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGCGTCA-GCCGTGCCGTGG 428
 QY 137 yLeuPheIleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValG 157
 Db 429 CTTTATTTATTTATTTTATTTTAAACACAGAGTGTACCACTCTTACCCAGGATGAGTGA 488
 QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluIleLys-HisProProAla 177
 Db 489 GTGGTGTGATCACAGCTCACTGCAGCTTCAACTCCTGAGATCAAGCAATCTCTCCTGCT 548
 QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIleP 197
 Db 549 CAGCTCCCAAGTAGCTGGGACCAAGACATGCACCACTACACCTGGTA-ATTTTATTTT 607
 QY 197 heIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
 Db 608 TTATTTTATTTTATTTTATTTTAAACACAGAGTGTCTAC-TCGTACCCAGGCTGGAGTGCAGTGGC 666
 QY 217 rgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerL 237
 Db 667 GCAATCTTGGCTCACTGCACCTCTGCTCCGGGTTCAAGTTATTTCTCTGCCCCAGCC 726
 QY 237 euLeuSerSerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeu 257
 Db 727 TCCTGAGTAGCTGGGACTACAGGCGCCACACGCTAGCTAATTTTGTATTATTTTAG 786
 QY 257 alGluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeu 276
 Db 787 TAGAGATGGGTTTCAACATGTTGCCAGGTTGATCTTGATCTCTTGACCTTGATCTG 846
 QY 277 ProAlaSerAla-SerGlnSerAlaGlyIleThrGly-ValSerHisHisAlaArgLeu 296
 Db 847 CTTGCTCGGCTACCCCAAGTGTGGGATTACAGGTCGTGACTCCAGCC---CGGCTTA 903
 QY 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnT 316
 Db 904 TTTTAAATTTTGTGTTTGAATGGAATCTCACTCTGTTACCCAGGTCGAGTGGAAT 963
 QY 316 rpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeu 336
 Db 964 GGCA-AATCTCGGCTACTCGCAACCTCTGCTCCCGGGTC-AAGGATTTCTCTGCTCA 1021
 QY 336 erLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIleP 356
 Db 1022 GCCTCCCAAGCAGCTGGGATTACGGAC-CTGCA-CCACACCCCGCTAATTTTGTATT 1079
 QY 356 heIleArgGlyValSerProTyrLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
 Db 1080 TCATTAGAGCGGGTTTA--CCATATTTGTGAGCTGGGCTCAAACTCTCAGCTCAGC 1137

Alignment Scores:

Pred. No.: 1,31e-108 Length: 1381

Score: 1517.00 Matches: 343

Percent Similarity: 90.16% Conservative: 5

Best Local Similarity: 88.88% Mismatches: 25

Query Match: 74.58% Indels: 22

DB: 2 Gaps: 3

US-09-380-203-2 (1-375) x AAQ77883 (1-1381)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20

Db 14 ATGGAGTTTTCGCTCTTGTGTCAGGCTGGAGTGCATGGCGCAATCTCAGCTCACGCC 73

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RESULT 11
AAT27765
ID AAT27765 standard; cDNA; 1381 BP.
XX AC AAT27765;
XX AC AAT27765;
DT 14-NOV-1996 (first entry)
XX AD 10-7 human neural thread protein clone (partial sequence).
DE Neutral thread protein; NTP; diagnosis; detection; Alzheimer's disease;
XX neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment; ds.
XX Homo sapiens.
OS
XX WO9615272-A1.
PN
XX 23-MAY-1996.
PD
XX 14-NOV-1995; 95WO-US017111.
PF
XX 14-NOV-1994; 94US-00340426.
PR
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX De La Monte S, Wands JR;
XX WPI; 1996-259865/26.
DR
XX Detection of neural thread protein in diagnosis of Alzheimer's disease -
PT also NTP DNA and protein sequences used in gene and anti:sense therapy.
XX Example 4c; Fig 16R; 238pp; English.
XX
CC A method for detecting the presence of neural thread protein (NTP) having
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
CC comprises (a) contacting a sample from a human subject that is suspected
CC of containing the NTP with at least one molecule capable of binding to
CC the protein; and (b) detecting any of the molecule bound to the protein.
CC The binding molecule is selected from an antibody free of natural
CC impurities, a monoclonal antibody or a binding fragment of either of
CC these. The method may be used for diagnosing the presence of Alzheimer's
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.
CC A number of clones of neural thread protein were isolated from healthy 17
CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex
CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
CC
XX SQ Sequence 1381 BP; 295 A; 385 C; 301 G; 400 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.31e-108 Length: 1381
Score: 1517.00 Matches: 343
Percent Similarity: 90.16% Conservative: 5
Best Local Similarity: 88.86% Mismatches: 25
Query Match: 74.58% Indels: 22
DB: 2 Gaps: 3

US-09-380-203-2 (1-375) x AAT27765 (1-1381)
QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
DB 14 ATGGAGTTTTCGGCTCTTTGTTGCCAGCTGGAGTGCATGGCGCAATCTCAGCTACCCGC 73
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValaGlyIle 40
DB 74 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCCGCTCCCGAGTAGTGGGATT 133
QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
DB 134 ACAGGCATGTGCAC-CACGCTCGGCTAAATTTTGTATTTTGTATAGTAGAGTAGGAGTTT 192
QY 61 --LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspProSerValSerA 80
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Db 193 AACTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATCTCCCGTCTCGGC 252
QY 80 laSerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAla 97
XX :::::
Db 253 CTGCCCAAAGTGTCTGAGATT--ACAGGCATGAGCCACCATGCGCGGCTCTGCTGGCT 309
QY 98 AsnPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeu 117
Db 310 AATTTTGTGGTAGAAACAGGGTTTCACTGATGTTGCCCAAGCTGGTCTCTGAGACTCAA 369
QY 117 sglnSerThrCysLeuSerLeuProLyCysTrpAspTyrArgAlaAlaValProgl 137
Db 370 GCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTACAGCGCTCA-GCCGTGCTGG 428
QY 137 yLeuPheIleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValgl 157
Db 429 CCTTTTATTTTATTTTATTTTAAAGACACAGGTGTACCACCTCTTACCAGGATGAAGTGCA 488
QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluIleLys-HisProProAlaAs 177
Db 489 GTGGTGTGATCACAGCTCACTGCAGCTTCAACTCTGAGATCAAGCAATCTCTCGCT 548
QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIleP 197
Db 549 CAGCCTCCCAAGTAGCTGGACCAAGACATGCACACTACACCTGGTA-ATTTTATTT 607
QY 197 heIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpA 217
Db 608 TTATTTTAAATTTTGTAGACAGAGTCTCAC-TCTGTCAACCAGGCTGGAGTGCAGTGCC 666
QY 217 rgAsnLeuGlySerLeuGlnProLeuProGlyPheIysLeuPheSerCysProSerL 237
Db 667 GCAATCTTGGCTCACTGCACAACTCTGCTCCGGGTTCAAGTATTCTCTGCTCCCGAGCC 726
QY 237 euLeuSerSerTrpAspTyrArgArgProProArgLeuAlaAsnPhePheValPheLeuV 257
Db 727 TCCTGAGTAGCTGGAGCTACAGCGCCCAACACCGCTAGCTAATTTTGTATTTTAG 786
QY 257 algluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGlyProCysAspLeu 276
Db 787 TAGAGATGGGGTTTCAACATGTTCCAGGTTGATCTTGATCTCTTGACCTTGTGATCTG 846
QY 277 ProAlaSerAla-SerGlnSerAlaGlyIleThrGly-ValSerHisHisAlaArgLeu 296
Db 847 CTGCTCTCGGCTACCCAAAGTGTGGGATTACAGGTCTGACTCCAGC---CGGCCTA 903
QY 296 lePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyValGlnT 316
Db 904 TTTTAAATTTTGTGTTGTAATGGAAATCTCCTCTGTACCAGGTCGGAGTGCAAT 963
QY 316 tpProAsnLeuGlySerLeuGlnProLeuProGlyLeuIysArgPheSerCysLeuS 336
Db 964 GGCA-AACTCTCGGCTACTCGCAACCTCTGCTCCCGGGTCA-AAGCGATTCTCCTGTCTCA 1021
QY 336 erLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIleP 356
Db 1022 GCCTCCCAAGCAGCTGGGATTACGGGAC-CTGCA-CCACACCCCGCTAATTTTGTATTT 1079
QY 356 heIleArgGlyGlyValSerProTyrLeuSerGlyTrp-SerGlnThrProAspLeuArg 375
Db 1080 TCATTAGAGCGGGTTTA--CCATATTGTTCAGGCTGGGTCTCAAACTCTCACCTCAGC 1137

RESULT 12
ACN44450
ID ACN44450 standard; DNA; 75252 BP.
XX AC ACN44450;
XX AC ACN44450;
DT 18-NOV-2004 (first entry)
XX Human genomic sequence hCG27772.
XX
```

KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

OS Homo sapiens.

PN WO2003073826-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

XX 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 904; Opp; English.

XX The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published

XX SQ Sequence 75252 BP; 16571 A; 19384 C; 19541 G; 19756 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.17e-63 Length: 75252
Score: 964.50 Matches: 252
Percent Similarity: 52.09% Conservative: 22
Best Local Similarity: 47.91% Mismatches: 95
Query Match: 47.42% Indels: 161
DB: 11 Gaps: 12

US-09-380-203-2 (1-375) x ACN44450 (1-75252)

QY 4 SerLeuLeuProArgLeuGluCysAenGlyAlaIleSerProValAlaHisArgLeuArg 23
DB 2398 TCGCTCTTTTGGCCAGGCTGGAGTCAATGGCGCAATCTCGGCTCATGCAACCTCCGC 2457
QY 24 LeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMet 43
DB 2458 CTCGGGGTTCAGCACTTCTCTGCTCAGCTCCGAGTAGTGGGATTACAGCATG 2517
QY 44 CysThrHisAlaArgLeuIleLeuThrPheLeuValGluMetGluPheLeuHisVal 63
DB 2518 CGCCACACCGCCGGCTAATTTGTAT---TTTAA-GTAGAGATGGGGTTTCTCCATGTT 2573
QY 64 GlyGlnAlaGlyLeuLeuProThrSerAspAspProSerValSerAlaSerGlnSer 83
DB 2574 GGTACGGCTGGTCTCGAATCGGACCTCAGGTGATCCACCTGCCTCAGCCTCCCAAGT 2633
QY 84 AlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCys-----Gly 101
DB 2634 GCTAGAGCGGGTGAGCCAC-----CGGCG-CTGGCCGGTAATTTGTATTTTAGT 2686
QY 102 ArgAsnArgValSerLeuMetCysProSerTrp-----SerProGluLeuLysGlnSer 119
DB 2687 AGAGACGGGGTTTCGCCATGTTGGCCAGGCTGGTGTGAACCTCCTCAGCTCAGGTGATCC 2746

QY 120 ThrCysLeuSerLeuProLysCysTrpAspTyrArg---ArgAlaAlaValProGlyLeu 138
DB 2747 ACCACCTTGGCTCCCAAGTGTGGAATTACATGTGTAGCCACCACCATGCCGGCTGCT 2806
QY 139 PheIleLeu----- 141
DB 2807 TTTTCTCTTAACCTCTTTCTCCCACTTTAGTTAATGCAGTGTCTAAGGCTAATTCAT 2866
QY 142 -----PhePheLeuArgHis----- 146
DB 2867 TAAGTGTGTCTTAATAAATGTTATTCACCAACACATCTTTATTAGGACACCTGTTGTAT 2926
QY 146 ----- 146
DB 2927 GCCAGCACTGGGATAGAACATGAGCAATGTCTCCACCTTTCTGAAGCCTACAGTCTA 2986
QY 146 ----- 146
DB 2987 GTAGGAGACAAACACAAATAACAAGTTAATAGGAATGATTATTATTACTATTATTTTGAGAC 3046
QY 147 ArgCysProThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeuGlnPro 156
DB 3047 AGAGTCTCGCTCTGTACACAGGCTGGAGTGCAGTGCAGCAATCTCGGCTCACTGCAAGCT 3106
QY 167 SerThrProGluIle-LysHisProProAlaSerAlaSerGlnValAlaGlyThrLysAs 186
DB 3107 CCACCTCCGGGTTACGCCATCTCCGCTCAGCTCCGAGTAGCTGGGACTGCAGG 3166
QY 186 pMetHisIstYrThrTrpLeuIlePheIle----- 196
DB 3167 CATGGCCACCAACGCCAGCTAATTTTGTATTATTTAGTAGAAACGGGGTTTCCACCATGT 3226
QY 196 ----- 196
DB 3227 TGTCAGGATGCTCTTAACCTTGACCTCGTGATCTGCCACCTCAGCCTCCCAAAATG 3286
QY 196 ----- 196
DB 3287 CTGGGATTACAGGCATGAGCCACTGTGCTGGCCGGAATATTATTATTATTATTATTA 3346
QY 197 -PheIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTr 216
DB 3347 TTTTATTTTATTTTGTAGAGAGAGTCTCAC-TCGTGACCCAGGCTGGAGTGCAGTG 3405
QY 216 pArgAsnLeuGlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSe 236
DB 3406 GCATGATCTCGGCTCACTGCAAGCTCTGCTCTCGGTTTCATGCCATTTCTCTGCTCAG 3465
QY 236 rLeuLeuSerSerTrpAspTyrArgArg---ProProArgLeuAlaAsn-PhePhe--- 253
DB 3466 CTTCTGTAGTGTGGGACTACAGACGCCCGCCACACACCTGGGTCAATTTTTTTTTTTT 3525
QY 254 --ValPheLeuValGluMet-GlyPheThrMetPheAlaArgLeuIleLeuIleSerGly 272
DB 3526 ATATATTTTAGTAGAGATGGGTTTACCATTGTAGCCAGATGGTCTCGATCTCTCTCA 3585
QY 273 ProCysAspLeuProAlaSerAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis 292
DB 3586 CTTCTGTATCCACCCGCTCAGCCTCCCAAGTGTGGGATTTACAGGCATGAGCCACCT 3645
QY 293 AlaArg----- 294
DB 3646 GCCCGCCGAGAAATTTATTATTATCATCATGATGAGTGTCTTCTAGAAATGCTAAAAAAA 3705
QY 295 -----LeuIlePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAla 312
DB 3706 GATTTTATTTATTTTA-TTTTATTTTGTAGAGAGGAGTCTGTGTTCTGTCGCCAGGCT 3764
QY 313 GlyValGlnTrpProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPhe 332
DB 3765 GGAGTGAATGTTGGGATCTCAGCTCACTGCAACCTCCACCTCTCTGGGTTTGGAGTGATTC 3824

QY 333 SerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuProHisProAlaAsn 352
DB 3825 TCCTCCCTCAGCTCCCGAGTACCTGGGATTACAGGTGTGTGCCACCACTGGCTAAT 3884
QY 353 PheCysIlePheIleArg--GlyGlyValSerProTyrLeuSerGlyTyrSerGlnThr 371
DB 3885 TTTTGTATTTTGTAGTAGACAGCGGGGAGTTTACCATATGGCCAGGCTGGTCTGATCT 3944
QY 372 ProAspLeuArg 375
DB 3945 CCTGACCTCAGG 3956
RESULT 13
ABD32700/c
ID ABD32700 standard; DNA; 33362 BP.
XX
AC ABD32700;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated genomic DNA HD14-035.
XX
KW Human; ds; cancer-associated protein; gene; cytostatic; cancer;
KW leukaemia; lymphoma; CAP.
XX
OS Homo sapiens.
XX
FN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
(SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
XX
XX WPI; 2004-652914/63.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 16; seqid 265; 310pp; English.
XX

CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 33362 BP; 8042 A; 8668 C; 8695 G; 7957 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.8e-59 Length: 33362
Score: 901.00 Matches: 236
Percent Similarity: 52.97% Conservative: 23
Best Local Similarity: 48.26% Mismatches: 101
Query Match: 44.30% Indels: 134
DB: 13 Gaps: 9
US-09-380-203-2 (1-375) x ABD32700 (1-33362)
QY 6 LeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeuPro 25
DB 12760 CTGTTGCCAGCGCTGGAGTGTGTGATCTTGGCTCACCGCAAGCTCCACCTCCCG 12701
QY 26 GlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThr 45
DB 12700 GGTTCACGCCATTCTCCTGCCTCAGCTCCCGAGTAGTGGGACTAGAGGCGTCTGCCAC 12641
QY 46 HisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPheLeuHisValGlyGln 65
DB 12640 CATGCCAGCTAAATTTTGTGATATTTTATTAGACAGAGGGTTTCAACCATCTTAGCCAG 12581
QY 66 AlaGlyLeuGluLeuProThr----- 72
DB 12580 GATGTCTTGTATCTCTGACCTCGGTGATCTGCCCGCTCTCTAAAGTGTGGGAT 12521
QY 72 ----- 72
DB 12520 TACAGCGGTGAGCCACAGTGTCCGGCCTATTATTATTATTTTATAGACAGATCTT 12461
QY 72 ----- 72
DB 12460 ACTTTGTTGCCAGGTTGTAGTGCAGTGGCATAATCTTGGCTCACTGCAACCTCTGCCTC 12401
QY 73 -----SerAspAspProSerValSerAlaSerGlnSerAlaArgTyrArgThrGlyHis 90
DB 12400 CTTGGTTCAAGTGATCTCTCGCTCAGCTCCCAAGTAGCTGGGATACAGGCACCTAC 12341
QY 91 HisAlaArgLeuCysLeuAlaAsnPheCys-----GlyArgAsnArgValSerLeuMet 108
DB 12340 CACCA-----TGCTAGTAATTTTGTATTTTATTAGTAGATGGGTTTCGCCATGT 12288
QY 109 CysProSerTrpSer-----ProGluLeuLys-GlnSerThrCysLeuSerLeuProLys 126
DB 12287 TGGCAAGGCTGTGCTCTGAACCTCTGACCTCAGGTGATATCGGCCACCTCGGCTCCAAA 12228
QY 126 sCysTrpAspTyrArgAlaAlaValProGlyLeuPheIleLeuPheLeuArgHis 146
DB 12227 GTGCTGGGATTTACAGGTGTGACCACTGGGCCACGCCCATCTCTTTTTTTTAAAGACA 12168
QY 146 sArgCysProThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeuGlnPr 166
DB 12167 -GAGTCCTGCTCTGTCGCCAGCGTGGAGTGCAGTGGCATGATCTCGGCTCATCTGCAATC 12109
QY 166 sSerThrProGluIleLys-HisProProAlaSerAlaSerGlnValAlaGlyThrLysA 186
DB 12108 TCCACCTCTGGGTTTCAAGCTATTCTCTGCTCAGCTCCCGAGTAGCTGGGATTACAG 12049
QY 186 spMetHisHisTyrThrTrpLeuIlePheIlePheAsnPheLeuArgGlnSerL 206


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Db 12048 GCATGCCACCACCGCTCGCTGATTTTATT-----TTGACAGCGAGTC 12004
Qy 206 euAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGlnProLeuP 226
Db 12003 TCAC-TCTGTACCCAGGCTGGAGTGCATGGCGTATCTTTGCTCAGCTACACCTCCGC 11945
Qy 226 roProGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAspTyrArgArg- 245
Db 11944 CGCCGGATTCAAGCGATTCTTCTGCCTCAGCTCCGAGTAGCTGGGATTACAGGCATG 11885
Qy 246 --ProProArgLeuAlaAsnPhePheValPheLeuValGluMet-GlyPheThrMetPhe 264
Db 11884 TGCCACCAATGCCCGGCTAATT--TTGTATTTTAGTAGAGATGGGGTTTCCACCATGTTG 11827
Qy 265 AlaArgLeuLeuLeu----- 269
Db 11826 GCAAGCTGTCTTGAACCTCTGACCTCAGGTGATACCCCACTCGGCTCCCAAGTG 11767
Qy 269 ----- 269
Db 11766 CTGGGATTACAGGTGAGCCACTGCGCCAGCCGCCCTCTCTTTTAAAGACAG 11707
Qy 270 -----IleSerGlyProCysAspLeu 276
Db 11706 AGTCCTGCTCTGCGCCAGGCTGGAGTGCAGTGGCATGATCTCGCTCACTGCAACCTC 11647
Qy 277 -----ProAlaSerAlaSerGlnSerAlaGlyIleThrGly 288
Db 11646 CACCTCTGGGTTCAGCTATTCTCTGCTCAGCTCTCGTAGTGGGATTACAGGC 11587
Qy 289 ValSerHisHisAlaArgLeuLeuPheAsnPheCysLeuPheGluMetGluSerHisSer 308
Db 11586 ATGCCACCAACCGCTGGCTGATTTTAT-----TTTGACAGCGAGTCTCGCTCT 11537
Qy 309 ValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGlnProLeuProGly 328
Db 11536 GTCCACCGCTGGAGTGCAGTGGCATGATCTTGGCTCACTACAACCTCCGCCACCCGGA 11477
Qy 329 LeuLysArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuProPro 348
Db 11476 TTCAAGCGATTCTTCTGCTCAGCTCCGAGTAGCTGGGATTACAGGCAGCTGCCACCA 11417
Qy 349 HisProAlaAsnPheCysIlePheIleArgGlyGlyValSerProTyrLeuSerGlyTrp 368
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RESULT 14
ID ABQ88096/c
XX ABQ88096 standard; cDNA; 92638 BP.
AC ABQ88096;
XX
XX
DT 18-SEP-2002 (first entry)
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DE Human osteoblast differentiation related cDNA SEQ ID NO 3.
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KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathic; ss.
XX
OS Homo sapiens.
XX
XX WO200250301-A2.
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PD 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US048276.
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XX 18-DEC-2000; 2000US-0255882P.
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PR 24-APR-2001; 2001US-0285691P.
XX
PA (GENE-) GENE LOGIC INC.
PA (PROC ) PROCTER & GAMBLE CO.
XX
PI Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI Mertz L;
XX
XX WPI; 2002-557663/59.
XX
PT Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process.
XX
PS Claim 1; SEQ ID NO 3; 78pp + Sequence Listing; English.
XX
CC The invention relates to genes and their expression profiles are used
CC for: (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal
CC deposition of bone tissue, abnormal rate of osteoblast formation or
CC osteoporosis; or (c) treating or monitoring treatment of the conditions
CC cited in (b), or monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC induced abnormalities in bone formation or bone loss, conditions that
CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),
CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome
CC or fibrous dysplasia. The present sequence is that of an osteoblast
CC differentiation associated cDNA marker of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 92638 BP; 21460 A; 24572 C; 25235 G; 21371 T; 0 U; 0 Other;

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Pred. No.: 1.14e-57 Length: 92638
Score: 892.50 Matches: 239
Percent Similarity: 43.48% Conservative: 21
Best Local Similarity: 39.97% Mismatches: 99
Query Match: 43.88% Indels: 242
DB: 6 Gaps: 10

US-09-380-203-2 (1-375) x ABQ88096 (1-92638)
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2005, 19:31:42 ; Search time 164 Seconds
(without alignments)
901.901 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2034	100.0	375	9 US-09-964-666-2	Sequence 2, Appli
2	2034	100.0	375	9 US-09-964-412-2	Sequence 2, Appli
3	2034	100.0	375	10 US-09-964-667-2	Sequence 2, Appli
4	2034	100.0	375	10 US-09-872-968-2	Sequence 2, Appli
5	2034	100.0	375	10 US-09-964-678A-2	Sequence 2, Appli
6	2034	100.0	375	14 US-10-146-130-2	Sequence 2, Appli
7	2034	100.0	375	14 US-10-092-934-10	Sequence 10, Appl
8	2034	100.0	375	14 US-10-153-334-1	Sequence 1, Appli
9	2034	100.0	375	14 US-10-198-069-1	Sequence 1, Appli
10	2034	100.0	375	14 US-10-157-031-299	Sequence 299, App
11	2034	100.0	375	14 US-10-198-070-1	Sequence 1, Appli

12	2034	100.0	375	16 US-10-755-889-410	Sequence 410, App
13	2034	100.0	375	17 US-10-910-173-2	Sequence 2, Appli
14	734.5	36.1	361	9 US-09-995-494-107	Sequence 107, App
15	729	35.8	449	14 US-10-007-280A-140	Sequence 140, App
16	569	28.0	241	15 US-10-276-774-1834	Sequence 1834, Ap
17	517	25.4	213	15 US-10-296-115-911	Sequence 911, App
18	471	23.2	286	15 US-10-291-172-654	Sequence 654, App
19	471	23.2	286	15 US-10-221-278-654	Sequence 654, App
20	428.5	21.1	183	9 US-09-989-920-245	Sequence 245, App
21	407	20.0	361	15 US-10-276-774-1862	Sequence 1862, Ap
22	382.5	18.8	341	18 US-10-220-335-586	Sequence 586, App
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25	356.5	17.5	603	16 US-10-408-765A-140	Sequence 140, App
26	353.5	17.4	217	14 US-10-017-161-1956	Sequence 1956, Ap
27	353.5	17.4	217	15 US-10-292-798-1604	Sequence 1604, Ap
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30	332	16.3	108	14 US-10-078-090-143	Sequence 143, App
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37	308	15.1	93	14 US-10-205-428-486	Sequence 486, App
38	308	15.1	100	13 US-10-016-157A-187	Sequence 187, App
39	307	15.1	114	15 US-10-104-047-2423	Sequence 2423, Ap
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44	300.5	14.8	101	15 US-10-276-774-2026	Sequence 2026, Ap
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ALIGNMENTS

RESULT 1
US-09-964-666-2
; Sequence 2, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-666-2

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Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-964-412-2
; Sequence 2, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wanda, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-412-2

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Best Local Similarity 100.0%; Pred. No. 1e-184;
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RESULT 3
US-09-964-667-2
; Sequence 2, Application US/09964667
; Publication No. US20030033621A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wanda, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,667
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0609.4370000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 375 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-964-667-2

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 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Publication No. US20030050262A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R.
 ; TITLE OF INVENTION: Inhibition of Neurodegeneration
 ; FILE REFERENCE: 21486-047
 ; CURRENT APPLICATION NUMBER: US/09/872,968
 ; PRIOR FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent In Ver. 2.1
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 ; US-09-872-968-2

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 Best Local Similarity 100.0%; Pred. No. 1e-184;
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 DB 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360

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QY 301 LFEMESHVSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 360
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 DB 361 VSPYLSGWSQTPDLR 375

RESULT 5
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 ; Sequence 2, Application US/09964678A
 ; Publication No. US20030066097A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R.
 ; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
 ; TITLE OF INVENTION: Effective for the Treatment or Prevention of
 ; TITLE OF INVENTION: Alzheimer's Disease
 ; FILE REFERENCE: 0609.4370002
 ; CURRENT APPLICATION NUMBER: US/09/964,678A
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 09/380,203
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: PCT/US98/03685
 ; PRIOR FILING DATE: 1998-02-26
 ; PRIOR APPLICATION NUMBER: 60/038,908
 ; PRIOR FILING DATE: 1997-02-26
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: AD7C-NTP CDNA
 ; US-09-964-678A-2

Query Match 100.0%; Score 2034; DB 10; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1e-184;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLPLRLCNGAISAHNRLLPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLPLRLCNGAISAHNRLLPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60

QY 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGRNRVSLMCPSPSPBLKQST 120
 DB 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGRNRVSLMCPSPSPBLKQST 120

QY 121 CLSLPKCWDYRAAIVPGLFLLFHRHRCPTLTQDEVQWCDHSLQSPSTPEIKHPASASQ 180
 DB 121 CLSLPKCWDYRAAIVPGLFLLFHRHRCPTLTQDEVQWCDHSLQSPSTPEIKHPASASQ 180

QY 181 VAGTKDMHYTWLIFIFNFRLQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
 DB 181 VAGTKDMHYTWLIFIFNFRLQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240

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Db 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
Qy 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Db 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Qy 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Db 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Qy 361 VSPYLSGWSQTPDLR 375
Db 361 VSPYLSGWSQTPDLR 375
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RESULT 6

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US-10-146-130-2
; Sequence 2, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.00007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-2
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Query Match 100.0%; Score 2034; DB 14; Length 375;

Best Local Similarity 100.0%; Pred. No. 1e-184; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEFSLLLPLECNGAISAHNRNLRPGSSDPSASGVPAGITGCTHARLILYFFLVEMEF 60
Db 1 MEFSLLLPLECNGAISAHNRNLRPGSSDPSASGVPAGITGCTHARLILYFFLVEMEF 60
Qy 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRVSLMCPSPSPKQST 120
Db 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRVSLMCPSPSPKQST 120
Qy 121 CLSLPKCDYRRAAVPGLFILFRLHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
Db 121 CLSLPKCDYRRAAVPGLFILFRLHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
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Qy 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
Db 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
Qy 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Db 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Qy 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Db 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Qy 361 VSPYLSGWSQTPDLR 375
Db 361 VSPYLSGWSQTPDLR 375
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RESULT 7

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US-10-092-934-10
; Sequence 10, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
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; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-10
```

Query Match 100.0%; Score 2034; DB 14; Length 375;

Best Local Similarity 100.0%; Pred. No. 1e-184; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEFSLLLPLECNGAISAHNRNLRPGSSDPSASGVPAGITGCTHARLILYFFLVEMEF 60
Db 1 MEFSLLLPLECNGAISAHNRNLRPGSSDPSASGVPAGITGCTHARLILYFFLVEMEF 60
Qy 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRVSLMCPSPSPKQST 120
Db 61 LHVGQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRVSLMCPSPSPKQST 120
Qy 121 CLSLPKCDYRRAAVPGLFILFRLHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
Db 121 CLSLPKCDYRRAAVPGLFILFRLHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
Qy 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
Db 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSS 240
Qy 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Db 241 WDYRRPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
Qy 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Db 301 LFEMESHVTOAGVQWPNLGSLOPLPPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Qy 361 VSPYLSGWSQTPDLR 375
Db 361 VSPYLSGWSQTPDLR 375
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RESULT 8

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US-10-153-334-1
; Sequence 1, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
```

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; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 59003-00006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-1
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Query Match 100.0%; Score 2034; DB 14; Length 375;

Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60

QY 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120
DB 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120

QY 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180

QY 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240
DB 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240

QY 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300

QY 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360

QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 9
US-10-198-069-1
; Sequence 1, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-1

Query Match 100.0%; Score 2034; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60

QY 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120
DB 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120

QY 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180

QY 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240
DB 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240

QY 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300

QY 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360

QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 10
US-10-157-031-299
; Sequence 299, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 299
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-299

Query Match 100.0%; Score 2034; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNGAISAHNRNLRPGSSDSPASASPVAGITGCMCTHARLILYFFLVEMEF 60

QY 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120
DB 61 LHVGAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRRVSLMCPSPSPKOST 120

QY 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCWDYRAAIVPGLFILFLLHRCPRTLQDEVQVCHSSLOPSTPEIKHPPASASQ 180

QY 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240
DB 181 VAGTKDMHHYTWLIFIFNFRQSLNSVTQAGVQWRNLGSLQPLPGFKLFCPSCLSS 240

QY 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFFVFLVEMGFTMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300

QY 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVTOAGVQWRNLGSLQPLPGFKLFCPSCLSSWDYGHLPHPANFCIFIRGG 360

QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

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RESULT 11
US-10-198-070-1
; Sequence 1, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
; TITLE OF INVENTION: PETIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-1

Query Match      100.0%; Score 2034; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
QY 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGGRNVRSLMCPSPKQST 120
DB 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGGRNVRSLMCPSPKQST 120
QY 121 CLSLPKCDWYRAAVPGLFIFLFRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCDWYRAAVPGLFIFLFRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
QY 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLSLQPLPPGKLFSCPSLLSS 240
DB 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLSLQPLPPGKLFSCPSLLSS 240
QY 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
QY 301 LFEMESHVSTQAGVQWRNLSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVSTQAGVQWRNLSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 12
US-10-755-889-410
; Sequence 410, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
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; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 410
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-410

Query Match      100.0%; Score 2034; DB 16; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
QY 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGGRNVRSLMCPSPKQST 120
DB 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGGRNVRSLMCPSPKQST 120
QY 121 CLSLPKCDWYRAAVPGLFIFLFRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
DB 121 CLSLPKCDWYRAAVPGLFIFLFRHRCPTLTQDEVQWCDHSSLOPSTPEIKHPPASASQ 180
QY 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLSLQPLPPGKLFSCPSLLSS 240
DB 181 VAGTKDMHYTWLIFIFINFLRQSLNSVTQAGVQWRNLSLQPLPPGKLFSCPSLLSS 240
QY 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
DB 241 WDYRPPRLANFFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIFNFC 300
QY 301 LFEMESHVSTQAGVQWRNLSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
DB 301 LFEMESHVSTQAGVQWRNLSLQPLPPGKLFSCPSLLSSDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 13
US-10-910-173-2
; Sequence 2, Application US/10910173
; Publication No. US20050090441A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R
; APPLICANT: de la Monte, Suzanne M
; TITLE OF INVENTION: Inhibition of Neurodegeneration
; FILE REFERENCE: 21486-047
; CURRENT APPLICATION NUMBER: US/10/910,173
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/872,968
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-173-2

Query Match      100.0%; Score 2034; DB 17; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
DB 1 MEFSLLLPLECNCGAISAHNRNLRPGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
QY 61 LHVGQAGLELPTSDPSVSASQARYRTGHARLCLANFCGGRNVRSLMCPSPKQST 120
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Db      61  LRVQAGLELPTSDPSVSASQARYRTGHHARLCLANFCGRNRVSLMCPSPKQST 120
QY      121  CLSLPKCWDYRAAVALPGLFLLFRLHRCPTLTQDEVQCDHSLQSTPEIKHPPASASQ 180
Db      121  CLSLPKCWDYRAAVALPGLFLLFRLHRCPTLTQDEVQCDHSLQSTPEIKHPPASASQ 180
QY      181  VAGTKDMHYTWTLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGFKLFCSPSLSS 240
Db      181  VAGTKDMHYTWTLIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGFKLFCSPSLSS 240
QY      241  WDYRRPRLANPFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHARLIFNFC 300
Db      241  WDYRRPRLANPFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHARLIFNFC 300
QY      301  LFEMESHVSTQAGVQWRNLGSLQPLPPGFKLFCSPSLSS 360
Db      301  LFEMESHVSTQAGVQWRNLGSLQPLPPGFKLFCSPSLSS 360
QY      361  VSPYLSGWSQTPDLR 375
Db      361  VSPYLSGWSQTPDLR 375

```

RESULT 14

```

US-09-995-494-107
; Sequence 107, Application US/09995494
; Patent No. US20020127578A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; APPLICANT: Chen, Sei-Yu
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0293
; CURRENT APPLICATION NUMBER: US/09/995,494
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,176
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-995-494-107

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Query Match      36.1%; Score 734.5; DB 9; Length 361;
Best Local Similarity 43.1%; Pred. No. 4,3e-61;
Matches 185; Conservative 24; Mismatches 93; Indels 127; Gaps 12;

QY      6  LLPRLECNAGISAHRNLRPGSSDPSASQSPVAGITGM-----CTHARL----- 49
Db      1  LLPRLECSGTIMACHCKLLGSGDLPASASRVGGITGMGTGSCAHHQIGLFPVAN 60
QY      50  -----ILYFFLVEMEFHVQAGLELPTSDPSVSASQARYRTGHHARLCL 97
Db      61  PERSFYILGTSPLDOLWLNMYF-----FALLIHIVLFL- 94
QY      98  NFGCRNRVLMCP--SWSPELKQSTCLSLPKCWDYRAAVALPGLFLLFRLHRC----- 148
Db      95  -----NRDSCCPGASLTGLGFAFACLSLPKCWDYTYGELL-LPIDIFLQVCCLSFYFLN 148
QY      149  PTLTQDEVQCDHSLQSTPEIKHPPASASQAGITGVSHARLIFNFC 208
Db      149  TVFQRAEV-----LIFFQVYVLAWSLHS 172
QY      209  VTOAGVQWRNLGSLQPLPPGFKLFCSPSLSSWDYRR--PPRLAN--FFVFLVEMGFTMPA 265

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Db      173  VAQAGVQWCMNLGSLQPLPPRFRFSCLSLSSWDHRRHAPPCLANFLFFKFLVDQSFTMLA 232
QY      266  RLILISGPC-DLPASASQAGITGVSH-----HARLIFNFCLEPES 306
Db      233  RVLVLSASGDDLPAPASQAGITGVHCTWPKSKFAUSHIGLAFHFAFFFFFAVAS 292
QY      307  HSVTQAGVQWPNLGLSLQPLPPGKRFSCLSLSSWDYHGLPHPPANFCIFIRGGVSPYLS 366
Db      293  HFIAQAGVQWRDLGSLQPLPPGFKQFLCLSLPGSDYRRAPRQANFCIFSRDGVSPCWT 352
QY      367  GWSQTPDLR 375
Db      353  GWSQTPDLR 361

RESULT 15
US-10-007-280A-140
; Sequence 140, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pr
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-140

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Query Match      35.8%; Score 729; DB 14; Length 449;
Best Local Similarity 42.6%; Pred. No. 1.9e-60;
Matches 196; Conservative 40; Mismatches 122; Indels 102; Gaps 19;

QY      6  LLPRLECNAGISAHRNLRPGSSDPSASQSPVAGITGMCTHARL-----ILYFFLVE 57
Db      1  LPFRLEYGGTILAYCNLHLPSSNPPTSASQVAGTRDVCCHTWTLCVCVCVCVCVCV 60
QY      58  MEFLHVQAGLELPTSDPSVSASQARYRTGHHARL-----LANFC----- 100
Db      61  MRHYVQAGLELSSDDPPIASASQAGIIGISH---CTWPMHDSFISPGAEPLTFAYTW 117
QY      101  -GRNRVSL-----MCPSPKQSTCLSLPKCWDYRR-----AAVPGI-----F 139
Db      118  PGRKIPITILLYPGDDVLVAFTELYYASPSQPGASDTARESWNGAVPDLHKEM 177
QY      140  ILFFLRHRCPTLTQDEV-----QWCD--HSSLQSTPEIKHPPA-----SASQVAGTKD 186
Db      178  LIF-----CPFSNQSHLWTKSKWAEVPHPGRRAPLPAKKEQKAANENSGSVTEPSSAS 232
QY      187  MHYTWLTFIFN-----FLRQSLNSVTQAGVQW---RNLSLQPLPPGFKLFCSPSLSS 239
Db      233  ILHARWDYV-FLINALIYFLRQSLNSVAQAGVQWQSGADLGLSLQPLPPGKAFPCLSL 291
QY      240  SWDYRR--PPRLANPFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHAR---- 294
Db      292  SWDYRR--PPRLANPFVFLVETGHHISQ--ISISAFCDPPASASQAGITGVSHAR---- 350
QY      295  -----LIFNFCLEFEMESHVTOAGVQWPNLG-----SLQPLPPGKRFSC 334
Db      351  YVSVGKQRCVYLFVFFFTETESTRTVAQAG--RLERSGAISTRRSLQPLPPGKRFSC 409
QY      335  LSLSSWDYHGLPHPPANFCIFIRGGVSPYLSGWSQTPDL 374
Db      410  LSLSSWDYRCTPPRLAHFCTFSRDGVSPCWGWSLSPDL 449

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Search completed: September 13, 2005, 19:38:05
Job time : 166 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2005, 19:32:27 ; Search time 43 Seconds
(without alignments)
651.009 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLLPRLECNCAISAHRLPGSSDSDSPASPVAGITGMCTHARLILYFFLVAMEF 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	100.0	375	2	US-08-454-557C-121
2	2034	100.0	375	2	US-08-340-426D-121
3	2034	100.0	375	2	US-08-450-673C-121
4	2034	100.0	375	4	US-09-872-968-2
5	1415.5	69.6	397	5	PCT-US95-17111A-121
6	267.5	13.2	96	4	US-09-513-999C-6065
7	259.5	12.8	144	4	US-09-513-999C-6953
8	256	12.6	108	4	US-09-513-999C-7878
9	254.5	12.5	239	4	US-09-800-729-193
10	254.5	12.5	310	4	US-09-800-729-193
11	253	12.4	118	4	US-09-663-600A-114
12	251	12.3	776	4	US-10-020-079-24
13	251	12.3	789	4	US-10-020-079-22
14	251	12.3	863	4	US-10-020-079-32
15	251	12.3	876	4	US-10-020-079-30
16	251	12.3	889	4	US-10-020-079-20
17	251	12.3	895	4	US-10-020-079-18
18	251	12.3	976	4	US-10-020-079-28
19	251	12.3	982	4	US-10-020-079-26
20	250	12.3	97	4	US-09-513-999C-4770
21	250	12.3	132	4	US-09-636-215-573
22	250	12.3	132	4	US-09-685-166A-573
23	250	12.3	132	4	US-09-679-426-573
24	250	12.3	132	4	US-09-759-143-573
25	250	12.3	132	4	US-09-651-236-573
26	250	12.3	135	4	US-09-685-166A-884
27	250	12.3	135	4	US-09-679-426-884

28	250	12.3	135	4	US-09-759-143-884	Sequence 884, App
29	247.5	12.2	112	4	US-09-513-999C-7870	Sequence 7870, App
30	246	12.1	119	4	US-09-513-999C-7867	Sequence 7867, App
31	245	12.0	102	4	US-09-621-976-6112	Sequence 6112, App
32	242.5	11.9	121	4	US-09-513-999C-7874	Sequence 7874, App
33	241	11.8	91	4	US-09-621-976-5929	Sequence 5929, App
34	229	11.3	84	4	US-09-621-976-7167	Sequence 7167, App
35	226	11.1	61	4	US-09-513-999C-4581	Sequence 4581, App
36	224.5	11.0	396	4	US-09-949-016-6783	Sequence 6783, App
37	224.5	11.0	442	4	US-09-949-016-9762	Sequence 9762, App
38	223.5	11.0	87	4	US-09-621-976-5968	Sequence 5968, App
39	219	10.8	76	4	US-09-621-976-6338	Sequence 6338, App
40	218	10.7	1079	3	US-09-058-489-22	Sequence 22, Appl
41	217.5	10.7	87	4	US-09-205-258-342	Sequence 342, App
42	216	10.6	169	4	US-09-663-600A-208	Sequence 208, App
43	215.5	10.6	108	4	US-09-513-999C-4433	Sequence 4433, App
44	214.5	10.5	83	4	US-09-621-976-5396	Sequence 5396, App
45	211.5	10.4	103	4	US-09-513-999C-5327	Sequence 5327, App

ALIGNMENTS

RESULT 1

US-08-454-557C-121
; Sequence 121, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0809.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-454-557C-121

Query Match 100.0%; Score 2034; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.2e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEFSLLPRLECNCAISAHRLPGSSDSDSPASPVAGITGMCTHARLILYFFLVAMEF	60
Db	1	MEFSLLPRLECNCAISAHRLPGSSDSDSPASPVAGITGMCTHARLILYFFLVAMEF	60
Qy	61	LHVQAGLELTPSDPSVSASQSAARYTGTGHARLCLANFCGRNVRVSLMCPSPSPKQST	120

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Db      61  LVHQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPWSPKQST 120
QY      121  CLSLPKCWYDRAAIVPGLFILFHLRHRCPTLTQDEVQVQWCHSSLOPSTPEIKHPPASASQ 180
Db      121  CLSLPKCWYDRAAIVPGLFILFHLRHRCPTLTQDEVQVQWCHSSLOPSTPEIKHPPASASQ 180
QY      181  VAGTKDMHHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLSLOPLPPGPKLFCPSCLSS 240
Db      181  VAGTKDMHHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLSLOPLPPGPKLFCPSCLSS 240
QY      241  WDYRPPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIENFC 300
Db      241  WDYRPPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIENFC 300
QY      301  LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
Db      301  LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
QY      361  VSPYLSGWSQTPDLR 375
Db      361  VSPYLSGWSQTPDLR 375

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RESULT 2
US-08-340-426D-121
; Sequence 121, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-426D-121

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Query Match      100.0%; Score 2034; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.2e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEFSLLLPLECNGAISAHRNLRPLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEF 60
Db      1  MEFSLLLPLECNGAISAHRNLRPLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEF 60

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QY      61  LVHQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPWSPKQST 120
Db      61  LVHQAGLELPTSDPSVSASQARYTGHARLCLANFCGRNRYSLMCPSPWSPKQST 120
QY      121  CLSLPKCWYDRAAIVPGLFILFHLRHRCPTLTQDEVQVQWCHSSLOPSTPEIKHPPASASQ 180
Db      121  CLSLPKCWYDRAAIVPGLFILFHLRHRCPTLTQDEVQVQWCHSSLOPSTPEIKHPPASASQ 180
QY      181  VAGTKDMHHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLSLOPLPPGPKLFCPSCLSS 240
Db      181  VAGTKDMHHYTWLIFIFIFNLRQSLNSVTQAGVQWRNLSLOPLPPGPKLFCPSCLSS 240
QY      241  WDYRPPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIENFC 300
Db      241  WDYRPPRLANFVFLVEMGFTMFARLILISGPCDLPASASQAGITGVSHHARLIENFC 300
QY      301  LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
Db      301  LFEMESHVSQTQGVQWPNLGSLOPLPPGLKRFSCSLPSSWDYGHLPHPANFCIFIRGG 360
QY      361  VSPYLSGWSQTPDLR 375
Db      361  VSPYLSGWSQTPDLR 375

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RESULT 3
US-08-450-673C-121
; Sequence 121, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-673C-121

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Query Match      100.0%; Score 2034; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.2e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEFSLLLPLECNGAISAHRNLRPLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEF 60
Db      1  MEFSLLLPLECNGAISAHRNLRPLPGSSDSPASASPVAGITGMCTHARLILYFFLVEMEF 60

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QY 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPKELKOST 120
 DB 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPKELKOST 120
 QY 121 CLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 DB 121 CLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 QY 181 VAGTKDMHHTWLIPIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLSS 240
 DB 181 VAGTKDMHHTWLIPIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLSS 240
 QY 241 WYRRPPRLANFVFLVEMGTFMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 DB 241 WYRRPPRLANFVFLVEMGTFMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 QY 301 LFEMESHSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
 DB 301 LFEMESHSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
 QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375

RESULT 4

US-09-872-968-2
 ; Sequence 2, Application US/09872968
 ; Patent No. 6770797
 ; GENERAL INFORMATION:
 ; APPLICANT: Wanda, Jack R
 ; APPLICANT: de la Monte, Suzanne M
 ; TITLE OF INVENTION: Inhibition of Neurodegeneration
 ; FILE REFERENCE: 21486-047
 ; CURRENT APPLICATION NUMBER: US/09/872,968
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-872-968-2

Query Match 100.0%; Score 2034; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.2e-215; Indels 0; Gaps 0;
 Matches 375; Conservative 0; Mismatches 0;

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 DB 1 MEFSLLPLRLCNGAISAHNRLPLGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 QY 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPKELKOST 120
 DB 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCPSPKELKOST 120
 QY 121 CLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 DB 121 CLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPEIKHPASASQ 180
 QY 181 VAGTKDMHHTWLIPIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLSS 240
 DB 181 VAGTKDMHHTWLIPIFIFNLRQSLNSVTQAGVQWRNLGSLQPLPPGPKLFCPSLSS 240
 QY 241 WYRRPPRLANFVFLVEMGTFMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 DB 241 WYRRPPRLANFVFLVEMGTFMFARLILISGCDLPASASQAGITGVSHHARLIFNFC 300
 QY 301 LFEMESHSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360
 DB 301 LFEMESHSTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSWDYGHLPHPANFCIFIRGG 360

QY 361 VSPYLSGWSQTPDLR 375
 DB 361 VSPYLSGWSQTPDLR 375
 RESULT 5
 PCT-US95-17111A-121
 ; Sequence 121, Application PC/TUS9517111A
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; APPLICANT: Wanda, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
 ; TITLE OF INVENTION: Detection of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/17111A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/340,426
 ; FILING DATE: 14-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609.3840002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 121:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 397 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US95-17111A-121

Query Match 69.6%; Score 1415.5; DB 5; Length 397;
 Best Local Similarity 74.6%; Pred. No. 6.8e-147;
 Matches 285; Conservative 10; Mismatches 44; Indels 43; Gaps 7;

QY 1 MEFSLLPLRLCNGAISAHNRLPLGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 DB 1 MEFSLLPLRLCNGAISAHNRLPLGSSDSPASASPVAGITGCTHARLILYFFLVEMEF 60
 QY 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCP 110
 DB 61 LHVGAGLELPTSDPSVSASQARYTGHARLCLANFCGRRVSLMCP 110
 QY 111 SWSPKELKOSTCLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPE 170
 DB 111 SWSPKELKOSTCLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPE 170
 QY 171 -----IKHPASASQVAGTKDMHHTWLIPIFIFNLRQSLNSVTQAGVQWRNLGSLQPLP 226
 DB 171 SWSPKELKOSTCLSLPKCWDYRAAVPGLFILFLRHCPTLTQDEVQWCDHSSLOPSTPE 226
 QY 227 PGKLFKPCSLSSWDYRRPPRLANFVFLVEMGTFMFARLILISGCDLP 278
 DB 227 PGKLFKPCSLSSWDYRRPPRLANFVFLVEMGTFMFARLILISGCDLP 278
 QY 279 SASQAGITGVSHHARLIFNFC LFEMESHSTQAGVQWPNLGSLOPLPPGLKRFSCLSL 338

Db 282 --PKVLGLQDVTPPTARPIINFCLEFESHESVTOAGVQWENLGSLOLPPLPGLKRFSCLSLP 339
QY 339 SSWDYGHLPHPANFCIFIRGG 360
Db 340 SSWDYGHLPHTPLIFVFSLEAG 361

RESULT 6

US-09-513-999C-6065
; Sequence 6065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6065
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-513-999C-6065

Query Match 13.2%; Score 267.5; DB 4; Length 96;
Best Local Similarity 60.4%; Pred. No. 1.5e-21;
Matches 61; Conservative 3; Mismatches 22; Indels 15; Gaps 2;

QY 205 SLNSVTQAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWDYRRPPRLANFVFLVEMGFTWF 264
Db 2 SFTLVAQAGVQWRDLGSPPLPPGKRFSCPSLPSWDYRHPVLLPANLFLVEMGF--- 58

QY 265 ARLILISGPC-----DLPASQSAGITGVSHARLIF 297
Db 59 ----LHVGPAGLGLPTSGDLPASQSAGIIGVSHRSQPF 95

RESULT 7

US-09-513-999C-6953
; Sequence 6953, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6953
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 9
; OTHER INFORMATION: Xaa= * or Cys or Trp
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa=Leu or Met or Val

; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 110
; OTHER INFORMATION: Xaa=Asp or His or Asn or Tyr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 132
; OTHER INFORMATION: Xaa=Asn or Thr
US-09-513-999C-6953

Query Match 12.8%; Score 259.5; DB 4; Length 144;
Best Local Similarity 72.0%; Pred. No. 2e-20;
Matches 59; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

QY 3 FSLILPRLCNGAISAHNRILPGSSDSPASVPVAGITGMCTHARLILYPFLVEMFPLH 62
Db 23 FSLISPRPECNGVILAHNCNRLSGSTHSPVSASGVAGITGMHHAQLI-FXFLVETGPHH 81
QY 63 VQAGLELPTGDDPSVSASQSA 84
Db 82 VQAGLELLTSGDPPASASQSA 103

RESULT 8

US-09-513-999C-7878
; Sequence 7878, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7878
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
; OTHER INFORMATION: score 5.7
; OTHER INFORMATION: seq VVCCSCSWFFLFC/FV
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 56
; OTHER INFORMATION: Xaa= * or Cys or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 59
; OTHER INFORMATION: Xaa=Arg or Ser

; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 61
; OTHER INFORMATION: Xaa=Asp or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa=Ala or Glu or Gly or Lys or Met or Arg or Thr or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 64
; OTHER INFORMATION: Xaa= * or Leu

FEATURE:
NAME/KEY: UNSURE
LOCATION: 66
OTHER INFORMATION: Xaa=Asn or Tyr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 67
OTHER INFORMATION: Xaa= * or Tyr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 71
OTHER INFORMATION: Xaa=Pro or Ser
US-09-513-999C-7878

Query Match 12.6%; Score 256; DB 4; Length 108;
Best Local Similarity 66.7%; Pred. No. 3.2e-20;
Matches 54; Conservative 3; Mismatches 20; Indels 4; Gaps 3;
QY 297 FNFC-LFEMESHVTOAGVQWPNLGSLOPLPGLKRFCSLSPSSWDYGHLPHPAN--F 353
DB 14 FLFCFVEMESHVTOAGVQWRDLGSLQALPPGSPF-CLSLPSSWDYRCLPPSSANFFF 72
QY 354 CIFIRGGVSPYLSGNSQPD 374
DB 73 XIFXSXXVXPXPGWXSQSPDL 93

RESULT 9
US-09-800-729-193
Sequence 193, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 193
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-193

Query Match 12.5%; Score 254.5; DB 4; Length 239;
Best Local Similarity 64.2%; Pred. No. 1.5e-19;
Matches 61; Conservative 6; Mismatches 25; Indels 3; Gaps 3;
QY 1 MEPSLLL-PRLENCGAISAHNRLPGSSDSPASASPVAGITGMCTHARLILYFVLVME 59
DB 120 LRWSLTSPRLCSCSAISAHNRLPGSSNSPALASQVAGITGICHARQI-FVFLVETG 178
QY 60 FLHVGQAGLELPTSDPVSASQSAR-YRTGHAR 93
DB 179 FCHVGQAGLELLISGDSPASAFQSGAGIIGVSHR 213

RESULT 10
US-09-800-729-190
Sequence 190, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 190
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-190

Query Match 12.5%; Score 254.5; DB 4; Length 310;
Best Local Similarity 64.2%; Pred. No. 2.2e-19;
Matches 61; Conservative 6; Mismatches 25; Indels 3; Gaps 3;
QY 1 MEPSLLL-PRLENCGAISAHNRLPGSSDSPASASPVAGITGMCTHARLILYFVLVME 59
DB 191 LRWSLTSPRLCSCSAISAHNRLPGSSNSPALASQVAGITGICHARQI-FVFLVETG 249
QY 60 FLHVGQAGLELPTSDPVSASQSAR-YRTGHAR 93
DB 250 FCHVGQAGLELLISGDSPASAFQSGAGIIGVSHR 284

RESULT 11
US-09-663-600A-114
Sequence 114, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31 US3 CJP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 114
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -83...-1
NAME/KEY: UNSURE
LOCATION: 28,32
OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-114

Query Match 12.4%; Score 253; DB 4; Length 118;
Best Local Similarity 65.9%; Pred. No. 7.9e-20;
Matches 60; Conservative 3; Mismatches 24; Indels 4; Gaps 3;
QY 204 QSLNSVTOAGVQWPNLGSLOPLPGLKRFCSLSPSSWDYRPPRL-ANFFVFLVEMGPT 262
DB 5 QSFILVAGVQWRHLSLQLPPEFKGFCLSLPSSWDYRPPPCPAGFFVFLVETGLH 64
QY 263 MF--ARLILISGPCDLPASASQSAGITGVSH 291

Db 65 HVGAGLELLTS-CSPPASASQAATGVSH 94

RESULT 12
US-10-020-079-24
; Sequence 24, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; FILE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 776
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(776)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-020-079-24

Query Match 12.3%; Score 251; DB 4; Length 776;
Best Local Similarity 47.9%; Pred. No. 2e-18;
Matches 69; Conservative 9; Mismatches 38; Indels 28; Gaps 8;
QY 211 QAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWDYRR--PPRLANFFVFLVEMGFT-MFARL 267
Db 649 QAGVQWRDLGSLQPPPPRFKQFSCLSLPSRWYRHAPPHPAN-FVFLVETGFLHVEAGL 707
QY 268 -ILISGPCDLPASASQAGITGVSHHARLIFFNCLFEMESHVSVTQAGVQWPNLGSLOPLP 326
Db 708 ELLTSG--DLPASASQIAGITGVSHRAQP--EVCFEN-RKHTGQR----- 747
QY 327 PGLKRFSCLSLPSSWDYGHLPHP 350
Db 748 ---EQMVCAGSERAWMRDLPGRP 768

RESULT 13
US-10-020-079-22
; Sequence 22, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; FILE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 789
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT

; LOCATION: (1)...(789)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-020-079-22

Query Match 12.3%; Score 251; DB 4; Length 789;
Best Local Similarity 47.9%; Pred. No. 2e-18;
Matches 69; Conservative 9; Mismatches 38; Indels 28; Gaps 8;
QY 211 QAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWDYRR--PPRLANFFVFLVEMGFT-MFARL 267
Db 662 QAGVQWRDLGSLQPPPPRFKQFSCLSLPSRWYRHAPPHPAN-FVFLVETGFLHVEAGL 720
QY 268 -ILISGPCDLPASASQAGITGVSHHARLIFFNCLFEMESHVSVTQAGVQWPNLGSLOPLP 326
Db 721 ELLTSG--DLPASASQIAGITGVSHRAQP--EVCFEN-RKHTGQR----- 760
QY 327 PGLKRFSCLSLPSSWDYGHLPHP 350
Db 761 ---EQMVCAGSERAWMRDLPGRP 781

RESULT 14
US-10-020-079-32
; Sequence 32, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 863
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(863)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-020-079-32

Query Match 12.3%; Score 251; DB 4; Length 863;
Best Local Similarity 47.9%; Pred. No. 2.3e-18;
Matches 69; Conservative 9; Mismatches 38; Indels 28; Gaps 8;
QY 211 QAGVQWRNLGSLQPLPPGFKLFSCPSLLSSWDYRR--PPRLANFFVFLVEMGFT-MFARL 267
Db 736 QAGVQWRDLGSLQPPPPRFKQFSCLSLPSRWYRHAPPHPAN-FVFLVETGFLHVEAGL 794
QY 268 -ILISGPCDLPASASQAGITGVSHHARLIFFNCLFEMESHVSVTQAGVQWPNLGSLOPLP 326
Db 795 ELLTSG--DLPASASQIAGITGVSHRAQP--EVCFEN-RKHTGQR----- 834
QY 327 PGLKRFSCLSLPSSWDYGHLPHP 350
Db 835 ---EQMVCAGSERAWMRDLPGRP 855
RESULT 15
US-10-020-079-30
; Sequence 30, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian

```
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 876
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(876)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-020-079-30

Query Match      12.3%; Score 251; DB 4; Length 876;
Best Local Similarity 47.9%; Pred. No. 2.4e-18;
Matches 69; Conservative 9; Mismatches 38; Indels 28; Gaps 8;

QY 211 QAGVQWRNIGSLQPLPPGFKLFSCPSLLSSWDYRR--PPRLANFFVFLVEMGFT-MPEARL 267
Db 749 QAGVQWRDLGSLQPPPPRFKQFSCLSLPSWDYRHAPPHPAN-FVFLVETGFLHVEAGL 807
QY 268 -ILISGPCDLPASASQSGAGITGVSHARLIFFNCLFEMESHVSHTQAGVQWPNLGLSLQLPLP 326
Db 808 ELLTSG--DLPASASQIAGITGVSHRAQP--EVCFEN-RKHTGQR----- 847
QY 327 PGLKRFPSCLSLPSSWDYGHLPHP 350
Db 848 ---EQWVCAGSERAWMRDLQGRP 868

Search completed: September 13, 2005, 19:38:54
Job time : 44 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 15, 2005, 21:58:59 ; Search time 4030 Seconds
(without alignments)
3541.961 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLLPLRLCNGAISAH.....PIRGVSPYLSGWQTPLDLR 375

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-OUTFMT=plc -THRESH=500 -WAIT -DSPBLOCK=100 -LONGLOG
-USER=US09380203 @CNG_1_1_4352/runat_13092005_170811_11685 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	935.5	46.0	622	CA437412	UI-H-DT0-
2	830.5	40.8	2587	HS802453	AL157469 Homo sapi
3	801.5	39.4	549	BM996475	BM996475 UI-H-DT0-
4	800	39.3	3016	BC068461	BC068461 Homo sapi
5	722.5	35.5	1875	BC009270	BC009270 Homo sapi
6	708	34.8	1842	BC011119	BC011119 Homo sapi
7	698.5	34.3	4191	AL832992	AL832992 Homo sapi
8	695	34.2	2786	BC035101	BC035101 Homo sapi
9	671	33.0	4087	BC024593	BC024593 Homo sapi

10	670	32.9	2097	3	CR614786	CR614786 full-length
11	670	32.9	2777	3	HS802772	AL390133 Homo sapi
12	662	32.5	3021	3	BC032537	BC032537 Homo sapi
13	657	32.3	2874	3	BC047576	BC047576 Homo sapi
14	654.5	32.2	990	2	AW600804	AW600804 N26-20 Hu
15	646.5	31.8	3775	3	CR627381	CR627381 Homo sapi
16	645	31.7	6056	3	CR627178	CR627178 Homo sapi
17	642.5	31.6	2716	3	CR749867	CR749867 Homo sapi
18	620.5	30.5	2076	3	BC035510	BC035510 Homo sapi
19	611.5	30.1	3566	3	HS805040	AL833727 Homo sapi
20	610.5	30.0	3146	3	BC036603	BC036603 Homo sapi
21	608.5	29.9	8213	3	HS809169	BS649018 Homo sapi
22	604.5	29.7	857	3	BQ437943	BQ437943 AGENCOURT
23	603	29.6	628	6	CD690152	CD690152 EST6675 h
24	597.5	29.4	2044	3	BC037797	BC037797 Homo sapi
25	596	29.3	2509	3	BC036220	BC036220 Homo sapi
26	592.5	29.1	613	6	CD709038	CD709038 EST25565
27	589.5	29.0	1345	1	AV762220	AV762220 AV762220
28	587	28.9	1683	3	BC038849	BC038849 Homo sapi
29	583.5	28.7	895	5	BU603620	BU603620 AGENCOURT
30	582.5	28.6	5165	3	HS802888	AL512697 Homo sapi
31	581	28.6	811	5	BS643852	BS643852 DKF2p7810
32	577.5	28.4	910	5	BQ722917	BQ722917 AGENCOURT
33	575	28.3	5797	3	CR749233	CR749233 Homo sapi
34	573.5	28.2	3620	3	HS804841	AL833528 Homo sapi
35	573	28.2	946	5	BQ589903	BQ589903 AGENCOURT
36	571	28.1	725	7	CR789571	CR789571 DKF2p4591
37	571	28.1	766	2	BF381650	BF381650 601815637
38	570.5	28.0	935	5	BU838401	BU838401 AGENCOURT
39	570	28.0	746	4	BG431326	BG431326 602499916
40	570	28.0	1545	3	BC030737	BC030737 Homo sapi
41	568	27.9	6146	8	AQ839831	AQ839831 260113-C4
42	567.5	27.9	737	1	AV700545	AV700545 AV700545
43	567.5	27.9	767	1	AV700498	AV700498 AV700498
44	566.5	27.9	3143	3	HS805999	BS37892 Homo sapi
45	565.5	27.8	1809	3	CR604283	CR604283 full-length

ALIGNMENTS

RESULT 1
CA437412
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA437412 622 bp mRNA linear EST 08-NOV-2002
UI-H-DT0-avk-a-06-0-UI-s1 NCI CGAP DT0 Homo sapiens cDNA clone
UI-H-DT0-avk-a-06-0-UI 3', mRNA sequence.
CA437412 GI:24801832
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 622)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 11-305, >ALU (matched complement) 221-440, >ALU (matched
complement) 452-620, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..622
/organism="Homo sapiens"
FEATURES
source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DT0-avk-a-06-0-UI"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP DT0"
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP DT0 is a cDNA library containing the following
tissue(s): Metastatic Chondrosarcoma in Lung. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(adT)18 tail. The sequence tag for this library is
AACTGTTCCG.
TAG_TISSUE=Lung metastatic chondrosarcoma
TAG_LIB=UI-H-DT0
TAG_SEQ=AACTGTTCCG"

ORIGIN
Alignment Scores:
Pred. No.: 3,06e-58 Length: 622
Score: 935.50 Matches: 189
Percent Similarity: 93.14% Conservative: 1
Best Local Similarity: 92.65% Mismatches: 6
Query Match: 45.99% Indels: 8
DB: 6 Gaps: 2

US-09-380-203-2 (1-375) x CA437412 (1-622)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db |||||
QY 21 ArgGAGTTTTCGCTCTGTGTCAGGCTGGAGTGCAATGGCGCAATCTCAGCTCACGCG 81
Db |||||
QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
Db |||||
QY 82 AACCTCGGCTCCGGGTTACAGCGATTCTCTGCTCAGCTCCTCCTAGTAGTGGATT 141
Db |||||
QY 41 ThrGlyMetCysThrHisAlaArgIleLeuLeuTyrPhePheLeuValGluMetGluPhe 60
Db |||||
QY 142 ACAGGCATGTGCACACGCTCGGCTAAATTTGTATTTTGTATTTTGTATTTTGTATTTT 201
Db |||||
QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspProSerValSerAla 80
Db |||||
QY 202 CTCCTATGTTGGTCAGCTCGTCTCGAACTCCCGACCTCAGATGATCCTCCGCTCGGCC 261
Db |||||
QY 81 SerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAlaAs 98
Db |||||
QY 262 TCCCAAGTGCTGAGATT---ACAGGCATGAGCCACCATCGCGGCTCTGCTGGCTAA 318
Db |||||
QY 98 nPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuLysG 118
Db |||||
QY 319 TTTTGTGTAGAAAACAGGGTTTCACTGATGTTGCCCAGCTGGTCTCTCGAGCTCAAGC 378
Db |||||
QY 118 InSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArg--AlaAlaValProGl 137
Db |||||
QY 379 AGTCACCTGCTCAGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCCGCTGCTGG 438
Db |||||
QY 137 yLeuPheIleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGl 157
Db |||||
QY 439 CCTTTTATTTATTTTATTTTAAACACACAGGTTCCCACTCTTACCAGATGAATGCA 498
Db |||||
QY 157 nTrpCysAspHisSerSerLeuGlnProSerThrProGluIleLys-HisProProAlaAs 177
Db |||||
QY 499 GTGGTGTGATCATCAGCTCATCGAGCTTTCAACTCTCTGAGATCAAGCAATCTCTGCT 558
Db |||||
QY 177 erAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIleP 197
Db |||||

Db 559 CAGCTCCCAAGTAGCTGGACCAAGACATGCACCTACACCTGGCTAATTTTATTT 618
QY 197 he 197
Db ||
Db 619 TT 620

RESULT 2
HSM802453/c
LOCUS HSM802453 2587 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp761N0823 (from clone DKFZp761N0823).
ACCESSION AL157469
VERSION AL157469.1 GI:7018485
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2587)
AUTHORS Bloembergen, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,
Osanger, A., Fobo, G., Han, M. and Wiemann, S.
SOURCE The German cDNA Consortium
DIRECT SUBMISSION
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp761N0823) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761N0823
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
Location/Qualifiers
1..2587
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp761N0823"
/tissue_type="amygdala"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/notes="RAB member RAS oncogene family-like 5, N-terminus
truncated"
gene 1..2587
CDS /gene="DKFZp761N0823"
<3..284
/gene="DKFZp761N0823"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAH10693.1"
/db_xref="GI:50949389"
/translation="PSHRKEMEMVYCFVQPSLQDTQCMLIHHKPGSGDDKGLSL
SPPLNKLVLHNSLEDDPEIRMEFIKLYLSMSRSRDEMSINT"

ORIGIN
Alignment Scores:
Pred. No.: 7,69e-50 Length: 2587
Score: 830.50 Matches: 236
Percent Similarity: 49.34% Conservative: 26
Best Local Similarity: 44.44% Mismatches: 99
Query Match: 40.83% Indels: 175
DB: 3 Gaps: 13

US-09-380-203-2 (1-375) x HSM802453 (1-2587)

QY 1 MetGluPheSerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArg 20
Db |||||
QY 2566 ATGAGAGTTTGTG-CTCTGTGTTGCCAGGCTGGAGTGCATGGCAATCTCGGCTTACTGC 2508
Db |||||
```

QY 21 AsnLeuArgLeuProGlySerSerSerSerProAlaSerAlaSerProValAlaGlyIle 40
 DB 2507 AACCTCCGCTCCAGGTTACAGGATTCCTCTGCTCAGCTCCAGGTAGCTGGATT 2448
 QY 41 ThrGlyMetCysThrHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPhe 60
 DB 2447 ACAGGCAGCTGTACACGCCAGCTAATT--TTTGATTTTATTTAGTAGACGGGGTTT 2391
 QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
 DB 2390 CACCATGTTGGACAGCTGCTTGAACCTCCTGACCTCAGGATTTCCACCCGCTCAGAC 2331
 QY 81 SerGlnSerAla----- 84
 DB 2330 TCCCAAGGTGGGATTACAGCGTAAGCCACTGACCCCGCTCCAGGCTCAAGCAAT 2271
 QY 85 ArgTyrArgThrGlyHisAlaArg-----LeuCysLeuAla 97
 DB 2270 TCTTATGCCCTCAGC-CACATGAGTAGCTGGTATTACAGGTGTGTGCCAATGCTGGCG 2212
 QY 98 AsnPheCys-----GlyArgAsnArgValSerLeuMetCysProSerTrp----- 112
 DB 2211 AATTTTGTATTTTATGATAGATGGGGTTTCG-----CCATGTTGGCCAGGCTGT 2161
 QY 113 -----SerProGluLeuLysGlnSerThrCysLeuSerLeuProLysCysTrpAspTyr 130
 DB 2160 TCTTGAACCTCCGCTTCCATCAGTCTCCCATCTAGCTCCCAAGTGTGGGATTAC 2101
 QY 131 Arg-----ArgAlaAlaValProGlyLeuPheLeuPheLeuPheLeuArgHis 146
 DB 2100 AGGTGTGACCCACTGCACTGCCAGGCACTTCAATTTTTTTTTTTTTTTTGTCTGTCTCAC 2041
 QY 147 ArgCysProThrLeuThrGlnAspGluValGlnTyrCysAspHisSerSerLeuGlnPro 166
 DB 2040 -----CAGGCTGGAGTGCGAGTGTGGTGGTCTCGGCTCACTGCAGTC- 2000
 QY 167 SerThrProGluLeuLeuHisProProAlaSerAlaSerGlnValAlaGlyThrIysAsp 186
 DB 1999 TCCGCTCGCGGTTTCAGGC-AATCTGCTCACTCCCTCTGAGTAGCTGGGACTACAGGC 1941
 QY 187 MetHisHisTyrThrTrpLeuLeuPheLeuPheLeu----- 198
 DB 1940 ATGCCCCCACTGCGGCTAATTTTGTATTTTATTTAGCAGACAGCGGGTTTCACCATGTT 1881
 QY 198 ----- 198
 DB 1880 GGCAGGATGCTCGATCTGACCTGTGACCTGCTGCTCGGCTCCCAAGTGC 1821
 QY 199 -----Phe-AsnPheLeu----- 202
 DB 1820 TGGGATCAGCGGTTGAGCCACCAGCCAGCCAGGCACTTCAATTTTTTGTCTCTGTG 1761
 QY 202 ----- 202
 DB 1760 TGTCTCGGAATAACTGAGAAAGTGCCACAGTATTGATTTGGGGTTTACAAACATATTTTA 1701
 QY 203 -----ArgGlnSerLeuAsn----- 207
 DB 1700 GTGAGTAGGCAAAATTTCAAAATACAAATCTATGAATAAGGATCAAGTATACGTTTCA 1641
 QY 207 ----- 207
 DB 1640 GGCATTTTAAGTACCCAGGTTCCCTCATTTATCTGAGGAGGCGGAGCATATGAACCTTAT 1581
 QY 208 -----SerValTh 210
 DB 1580 TTAGACTTCTTCTAAACATTTAATGTAATTTAATTTATTTAGACAGGATGCTGTGTC 1521
 QY 210 rGlnAlaGlyValGlnTyrArgAsnLeuGlySerLeuGlnProLeuProGlyPheLeu 230
 DB 1520 CCAGGCTGAGTATAGTGGCGGATCTCGGCTCAGTGCAATCTCTGCTCCAGGCTCAA 1461

QY 230 sLeuPheSerCysProSerLeuLeuSerSerTrpAspTyrArgArgProPro-ArgLeuA 250
 DB 1460 GCAATTTCTTATGCTTCAGCCAGGAGTAGCTGGTATCACAGGCTGGCCCAACACACC 1401
 QY 250 laAsnPhePheValPheLeuValGluMetGly-PheThrMetPheAlaArgLeuLeuLeu 269
 DB 1400 TGTAAATTTTGTATTTTATGATAGACGGGATTTTGGCATGTTGGCCAGGCTGGCTCG 1341
 QY 270 lIleSerGlyPro--CysAspLeuProAlaSerAlaSerGlnSerAlaGlyIleThrGlyV 289
 DB 1340 AACTCCCGCTCAAGTATCGGCTGCTCAGCATCCCAAGTCTGGGATTACAGTG 1281
 QY 289 alSerHisHis-----AlaArgLeuIlePheAsnPheCysLeuPheGluMetGluSerH 307
 DB 1280 TGAGCCACCGCTCTCTGGCTAGAACTCTTTTTT-----TTTGAGATGGAGTCTT 1231
 QY 307 isSerValThrGlnAlaGlyValGlnTyrProAsnLeuGlySerLeuGlnProLeuProP 327
 DB 1230 GCTCTGTTGCCCAAGCTGGAGTACAGTGGCGCAATCTTTGGCTCACTGCCAACCTCTGCCTC 1171
 QY 327 roGlyLeuLysArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuP 347
 DB 1170 CCGGCTCAACAATCTTATGCTCAGCTCCCAAGTAGCTGGGATCACAGCAGCGCG 1111
 QY 347 roProHisProAlaAsnPheCysIlePheIleArgGlyValSerProTyrLeuSerG 367
 DB 1110 CACCACACCGCTGATTTTCTATTTTATGATAGATGGGTTTTCACCACGTTGGTCTAG 1051
 QY 367 lyTrpSerGlnThrProAspLeu 374
 DB 1050 GATGCTCTGATCTCTGACCTC 1028
 RESULT 3
 LOCUS BM996475 549 bp mRNA linear EST 17-JUN-2002
 DEFINITION UI-H-DT0-avl-i-16-0-UI.s1 NCI_CGAP_D10 Homo sapiens cDNA clone
 IMAGE:5881047 3', mRNA sequence.
 ACCESSION BM996475
 VERSION BM996475.1 GI:19721376
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Cloning Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 The following repetitive elements were found in this cDNA
 sequence: 11-305, >ALU (matched complement) 221-440, >ALU (matched
 complement) 243-535, >SVA#Other
 Seq primer: M13 FORWARD
 POLYA=Yes.
 FEATURES
 source Location/Qualifiers
 1..549
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5881047"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_D10"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker: Site 1: EcoR I; Site 2: Not I;
 NCI_GCAP_DT0 is a cDNA library containing the following
 tissue(s): Metastatic Chondrosarcoma in Lung. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pTV73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AACTCTTCGG.
 TAG_TISSUE=lung metastatic chondrosarcoma
 TAG_LIB=UI-H-DT0
 TAG_SEQ=AACTGTTTCGG"

ORIGIN

Alignment Scores:
 Pred. No.: 1,45e-48 Length: 549
 Score: 801.50 Matches: 165
 Percent Similarity: 92.18% Conservative: 0
 Best Local Similarity: 92.18% Mismatches: 6
 Query Match: 39.41% Indels: 8
 DB: 5 Gaps: 2

US-09-380-203-2 (1-375) x BM996475 (1-549)

QY 1 MetGluPheSerLeuLeuProArgLeuGluCyAsnGlyAlaIleSerAlaHisArg 20
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 Db 22 ATGGAGTTTTCGCTCTGTGTCAGGCTGGAGTGAATGGCGCAATCTCAGCTCACC 81
 |||||
 QY 21 AsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIle 40
 |||||
 Db 82 AACCTCCGCTCCCGGGTTCAAGCGATTCTCTGCTCAGCTCCCTAGTAGTGGGATT 141
 |||||
 QY 41 ThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPhe 60
 |||||
 Db 142 ACAGGATGTGCACACAGCTCGGCTGATTTGTTATTTTATTTAGTAGATGGAGTTT 201
 |||||
 QY 61 LeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAla 80
 |||||
 Db 202 CTCATGTTGGTCAGGCTGGTCTCGAACTCCGACCTCAGATGATCTCCGCTCTCGGCC 261
 |||||
 QY 81 SerGlnSerAlaArgTyrArgThrGly-----HisHisAlaArg-LeuCysLeuAlaAs 98
 |||||
 Db 262 TCCCAAAAGTGGTGGAGATT---ACAGGCATGAGCCACCATGCCCGGCTCTGCTGGCTAA 318
 |||||
 QY 98 nPheCysGlyArgAsnArgValSerLeuMet-CysProSerTrpSerProGluLeuLysG 118
 |||||
 Db 319 TTTTGTGTAGTAACAGGGTTTCACTGATGTGTCACAGCTGGTCTCTGAGCTCAAGC 378
 |||||
 QY 118 InSerThrCysLeuSerLeuProLysCysTrpAspTyrArgArg--AlaAlaValProGl 137
 |||||
 Db 379 AGTCACCTGCTCAGCTCCCAAGTGTGGGATTACAGGCGTGAGCCACCGCTGCTGG 438
 |||||
 QY 137 YleuPheHelleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGl 157
 |||||
 Db 439 CCTTTTATTTATTTATTTTATTTTAAAGACACAGGTTGCCACTCTTATCCAGGATGAAGTGA 498
 |||||
 QY 157 nTrpCysAspHisSerSerLeuGlnProSerThr-ProGluIleLys 172
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 Db 499 GTGGTGTGATCAGCTCACTGAGCCTTCACTCTGAGATCAAG 545
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RESULT 4

BC068461/c
 LOCUS BC068461 3016 bp mRNA linear HTC 19-JUL-2004
 DEFINITION Homo sapiens cDNA clone IMAGE:30342539, with apparent retained
 intron.
 ACCESSION BC068461
 VERSION BC068461.1 GI:46249759
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 3016)

REFERENCE

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Ditzchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smallwood,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

TITLE

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (02-APR-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael Brownstein / Ted Usdin
 Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 168 Row: m Column: 1
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 21361917
 This clone has the following problem: retained intron.

FEATURES

source

1..3016
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30342539"
 /tissue_type="Placenta, normal"
 /clone_lib="NIH MGC_147"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

ORIGIN

Alignment Scores:

Pred. No.: 1.53e-47 Length: 3016
 Score: 800.00 Matches: 216
 Percent Similarity: 57.51% Conservative: 29
 Best Local Similarity: 50.70% Mismatches: 103
 Query Match: 39.33% Indels: 81
 DB: 3 Gaps: 11

US-09-380-203-2 (1-375) x BC068461 (1-3016)

[illegible]

Qy	312	aGlyValGlnTrpProAsnLeuGlySerLeuGlnProLeuProProGlyLeuIysArgPh	332
Db	1983	TGGAGTGCAGTGGCACAATCTTGGCTCACCTGCAACCTCCACCTTCCAGGTTCAAGCTATT	1924
Qy	332	eSerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAs	352
Db	1923	CTCTTGCC--TCATGTCGAGTAGCTGGGAAATACGGTGGCTGCCACCATGCTCGGCTAA	1866
Qy	352	nPheCysIlePheIleArgGlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrPr	372
Db	1865	TTTTTGATTTTATGATGAGATGGGGTTTCACCATATTGGCCAGGCTGGTCTCAAACCTCC	1806
Qy	372	aAspLeuArg	375
Db	1805	TGACCTCAAG	1796

RESULT 5

BC009270	BC009270	1875 bp	mRNA	linear	HTC 04-MAR-2003
LOCUS					
DEFINITION	Homo sapiens, Similar to hypothetical protein PRO1722, clone				
	IMAGE:3342760, mRNA.				
ACCESSION	BC009270				
VERSION	BC009270.1	GI:14627272			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE

2. Straussberg R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

Contact: MGC help desk
 Email: cgapsb-x@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywnski, Reta Koffler, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeeadi, Jacqueline
 Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Scott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuverduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 22 Row: j Column: 8
This clone has the following problem: retained intron.

FEATURES source

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1. 2075
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3342760"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH MGC 16"
/lab_host="DH10B-R"
note="Vector: pOTB7"
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ORIGIN

Alignment Scores:		
Pred. No.:	3.69e-42	Length:
Score:	722.50	Matches:
		193
		1875

Percent Similarity:	52.82%	Conservative:	13
Best Local Similarity:	49.49%	Mismatches:	62
Query Match:	35.52%	Indels:	12
DB:	3	Gaps:	7

US-09-380-203-2 (1-375) x BC009270 (1-1875)

Qy	4	SerLeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArg	23
Db	576	TCGCTTTTGTTCGCCAGGCTGGAGTGCATGGCTCGATTTTCAGCTCAGCTGCACACCTTC	635
Qy	24	LeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMet	43
Db	636	CTGCGGGTTCAAGCGATTCTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCATG	695
Qy	44	CysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGluPheLeuHisVal	63
Db	696	TGCCACCATGCGCGCTAATTTGTG---CTTTTATTAGACAGCAGGTTTCTCCATGTT	751
Qy	64	GlyGlnAlaGlyLeuLeuLeuLeuProThrSerAspAspProSerValSerAlaSerGlnSer	83
Db	752	GGTCAGGCTGTGCTTGAACCTCCCGACCTCAGGTGATCCACC-----	792
Qy	84	AlaArgTyrArgThrGlyHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAsn	103
Db	792	-----	792
Qy	104	ArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSer	123
Db	793	-----TGCTCTCAGC	801
Qy	124	LeuProLysCysTrpAspTyrArgArgAlaAlaValProGlyLeuPheIleLeuPhePhe	143
Db	802	CTCCCAAGTGCTGGGATTACAGG-----	825
Qy	144	LeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSer	163
Db	826	-----CATGA-GCC	833
Qy	164	LeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSerGlnValAlaGly	183
Db	834	ACCATGCTCGCACT-----	848
Qy	184	ThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePheAsnPheLeuArg	203
Db	849	-----GGTTTTTTTGAGA	860
Qy	204	GlnSerLeuAsnSerValThrClnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGln	223
Db	861	TGGAAATCTCGT-TATGTCAACCCAGCTGGAGGCGAGTGGCAGACTCAGCTCAGCTGTA	919
Qy	224	ProLeuProProGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAspTyr	243
Db	920	CCTTTGCCGT--GGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTAC	977
Qy	244	ArgArg---ProProArgLeuAlaAsnPhePheValPheLeuValGluMet-GlyPheTh	262
Db	978	AGGCACGCTCCACCACACCCCGCTAATTTTTTGTATTATTAGTAGAGATGGGGTTTCAC	103
Qy	262	rMetPheAlaArgLeuIleLeuIleSerGlyPro--CysAspLeuProAlaSerAlaSer	281
Db	1038	CATATTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCGCTTGCCCTGGCCCTCC	109
Qy	282	GlnSerAlaGlyIleThrGlyValSerHisHisAlaArg-----LeuIlePhe	297
Db	1098	CAAAAGTGTGGGATTACAGGGGTGAGCCACCGTGCCCATCCAACCTTAACCTTTAATTTT	115
Qy	298	Asn-----PheCysLeuPheGluMetGluSerHis	307
Db	1158	TCTCATGTAAATTTGTTCAATTTCTTTTTTTTTTTTTTTTTTTTTTTGTGACAACTCTC	121
Qy	308	SerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGlnProLeuProPro	327

Db	1218	TGTCACCCCGACGCGCAGAGTGCGAGTCTCAACTCTGCAACCTCCACCCGCC	1217
Qy	328	GlyLeuIysArgPheSerCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuPro	347
Db	1278	GGGTCCCTGTGATTTTCCACACCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGTGGGCCA	1337
Qy	348	ProHisProAlaAsnPheCysIlePheIleArgGlyGlyValSerProTyrLeuSerGly	367
Db	1338	CCACACCGCGCTAATTTTGTGATTTTGTAGTAGACGGGGTTTCACCACATTGTCAGGC	1397
Qy	368	TrpSerClnThrProAspLeuArg	375
Db	1398	TGGTCTGAACACTCTGGCCTGAAG	1421
RESULT 6			
BC011119			
LOCUS	BC011119	1842 bp	mRNA
DEFINITION	Homo sapiens, clone IMAGE:3047997,		linear
ACCESSION	BC011119		
VERSION	BC011119.1		
KEYWORDS	GI:15029795		
SOURCE	HTC.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 1842)		
	Strausberg,R.		
	Direct Submission		
	Submitted (25-JUL-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk		
	Email: cgapsb-r@mail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Baylor College of Medicine Human Genome		
	Sequencing Center		
	Center code: BCM-HGSC		
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/		
	Contact: amg@bcm.tmc.edu		
	Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,		
	Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,		
	A.N., Gibbs, R.A.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 19 Row: 0 Column: 1
This clone has the following problem: retained intron.

FEATURES

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Best Local Similarity:	58.24%
Query Match:	34.81%
DB:	3
Length:	1842
Matches:	205
Conservative:	28
Mismatches:	90
Indels:	34
Gaps:	10

US-09-380-203-2 (1-375) x BC011119 (1-1842)

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 Db 598 CTGTCGCCAGGCTGAGTGCATGCTGGCTTACTCGCAAGCTCCGCTCCCG 657
 QY 26 GlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThr 45
 Db 658 GGTTCACACTTCTCTCGCTCAGCTCCAGTCTCCAGTAGCTGGGACTACTGGTCCGCCAC 717
 QY 46 HisAlaArgLeuIleLeuThrPheLeuValGluMetGluPheLeuHisValGlyGln 65
 Db 718 CAGCGCCGCTAATTTT-TTCTATTTTAGTAGACGGGTTTCCACGCTGTAGCCAG 776
 QY 66 AlaGlyLeuGluLeuProThr-SerAspSerProSerValSerAlaSerGlnSerAlaAr 85
 Db 777 GATGGTCTTGATGCTGCTGACCTTGATTCACCTGCC---TCGGCTCCCAAGTCTGG 833
 QY 85 gTyrArgThrGly-----HisAlaArg-LeuCysLeuAlaAsnPheCysGlyArgA 103
 Db 834 GATT---ACAGGAGTGAGCCCGCGCGCTTATTTTA-----TTTTTAATAGAG 884
 QY 103 snArgValSerLeuMetCysPro-----SerTrpSerProGluLeuLysGlnSerThrC 121
 Db 885 AT---GTCTCATATGTCGCGGACTAGTCTCAAACTCTGGGCTCAGACCATCTCTCC 941
 QY 121 ysLeuSerLeuProLysCysTrpAspTyrArgArg--AlaAlaValProGlyLeuPheI 140
 Db 942 A-CTGGCCCTCCCAAGTCTGGGATTACAGTTCTGAGCCACTGTGCTGGCTGGCTCTTT-- 998
 QY 140 eleuPheLeuArgHisArgCysProThrLeuThrGlnArgGluValGlnThrCysAs 160
 Db 999 ----TTTTTTTGTAGATA-GAATCTCCCTCTGTACCCAGGTGGACTGCTGGTGGCA 1053
 QY 160 phiSerSerLeu-----GlnProSerThrProGluIleLys-H 173
 Db 1054 TCTAGCTCACTGCACCTCGCTAGTTCAGCGCACTCTCGTCTCTGGTTCAGCA 1113
 QY 173 isProProAlaSerAlaSerGlnValAlaGlyThrLysAspMethHisIstYrThrTrpL 193
 Db 1114 ATTCTCTGCTCCAGCTCCGAGTAGCTGAGATTACAGGCGCATGTCACCCAGCTGCG 1173
 QY 193 euIlePheIlePheIlePheAsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaG 213
 Db 1174 TAAATTTTGT 1229
 QY 213 lyValGlnTrpArgAsnLeuGlySerLeuGlnProLeuProProGlyPheLysLeuPheS 233
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 QY 233 erCysProSerLeuLeuSerSerTrpAspTyrArgArgProPro-ArgLeuAlaAsnPhe 252
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 QY 292 sAlaArgLeuIlePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAl 312
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 Db 1520 GGGAGTCCAGTGGCGGTGATCTTTGGTCACTGCAACCGCGCGCTCCCGGTTCAAGCAATT 1579
 QY 332 eSerCysValSerLeuProSer 339
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 LOCUS Homo sapiens mRNA; cDNA DKFZp666K083 (from clone DKFZp666K083).
 ACCESSION AL832992
 VERSION AL832992.1 GI:21733581
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 4191)
 AUTHORS Ansong,W., Krieger,S., Regiert,T., Rittmuller,C., Schwager,B.,
 Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
 Wiemann,S.
 CONSRM The German cDNA Consortium
 TITLE Direct Submission
 JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 COMMENT Neuherberg, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratories,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 This clone (DKFZp666K083) is available at the RZPD Deutsches
 Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
 Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp666K083
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
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 Best Local Similarity: 42.95% Mismatches: 92
 Query Match: 34.34% Indels: 135
 DB: 3 Gaps: 11
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 Db 2876 CTGTGCGCTAGCTGAGTGCAGGCGTCCGATCTCGGCTCACTGCAACCTCCGCTCCCG 2817
 QY 26 GlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThr 45
 Db 2816 GGTTCACACTTCTCTCGCTCAGCTCCCAAGTAGCTGGACTACAGGCGCGTGCAC 2757
 QY 46 HisAlaArgLeuIleLeuThrPheLeuValGluMetGluPheLeuHisValGlyGln 65
 Db 2816 GGTTCACACTTCTCTCGCTCAGCTCCCAAGTAGCTGGACTACAGGCGCGTGCAC 2757

D	b		2756	TACACCGGCTAAATTTTCTGGCAATTTTTTAATAGAGACAGGGTTTCGCCATTGTGGCCAG	2697
Q	y	66	AlaGlyLeuGluLeuProThrSerAspAspProSerValSerAlaSerGlnSerAlaArg	85	
D	b	2696	GCTGATCTCAAACCTCCTGGCCTCATCTGAT-----	2667	
Q	y	86	TyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCysGlyAArgAsnArgVal	105	
D	b	2667	-----	2667	
Q	y	106	SerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSerLeuPro	125	
D	b	2666	---:CGCC-CCC-----CTTGGCTCCCCA	2647	
Q	y	126	LysCysTrpAspTyrArgArg--AlaAlaValProGlyLeuPheIleLeuPhePheLeuA	145	
D	b	2646	AAGTCTGGGATTACAGCGGTGACGCCACCACGATCCCGGCCTCCCTTATGTTTGATCGAG	2587	
Q	y	145	rgHis-----	149	
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Q	y	149	roThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeuGlnProSerThrP	169	
D	b	2526	TAGTCATCATGACAGGATCCCTTCAATGGGGGAG-----TCATGTC	2485	
Q	y	169	roGluIleLysHisProProAlaSerAlaSerGlnVal-----	181	
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D	b	2424	CCCTTCATTCTTTTCTTGGAGTCAGATG-TTGAACCTTCTCGAATTGGTCATCTAAT	2366	
Q	y	193	-----LeullePheIle-----	196	
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Qy	351	aAsnPheCysAilePheIleArgGlyGlyValSerProTyrLeuSerGlyTrpSerGlnTh	371
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DEFINITION	Homo sapiens, Similar to neuronal thread protein, clone IMAGE:5262055, mRNA.	2786 bp	mRNA linear HTC 04-MAR-2003
ACCESSION	BC035101		
VERSION	BC035101.1	GI:23272462	
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2786)		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
REMARK	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapsb-x@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbio.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
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Best Local Similarity:	44.66%	Mismatches:	77
Query Match:	34.17%	Indels:	131
DB:	3	Gaps:	9
US-09-380-203-2 (1-375) x BC035101 (1-2786)			
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Db	1371	CCCAGCGTGAGTGCACTGGCACNAUCTTGGCTCATGTGCCACTTCCACTTCCAGGTTC	1430
Qy	28	SerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThrHisAla	47

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 2196 GGTTCAGCAATCT 2255
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366 SerGlyTrpSerGlnThrProAspLeuArg 375
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 JOURNAL
 REMARK
 COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdepaxil.stanford.edu
 R. M.
 Clon distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 22 Row: m Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
 This clone has the following problem: retained intron.
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ORIGIN

Alignment Scores:

Pred. No.: 2,79e-38 Length: 2097
Score: 670.00 Matches: 177
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Best Local Similarity: 47.20% Mismatches: 77
Query Match: 32.94% Indels: 103
DB: 3 Gaps: 5

US-09-380-203-2 (1-375) x CR614786 (1-2097)

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QY 26 GlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThr 45
DB 486 GTTCAAGTATCTCTCCCTCAGCTTCTGAGTGTGGATTATAGCGCATGCCAC 545
QY 46 HisAlaArgLeuIleLeuThrPhePheLeuValGluMetGluPheLeuHisValGlyGln 65
DB 546 CATGCTGGCTAATT---TTTGTATTTTAAATAGAGACGGAGTTCACCATCTGTGTCAG 602
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QY 105 ValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSerLeu 124
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DB 701 ----- 701
QY 145 ArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCysAspHisSerSerLeu 164
DB 701 ----- 701
QY 165 GlnProSerThrProGluIleLysHisProProAlaSerAlaSerGlnValAlaGlyThr 184
DB 701 ----- 701
QY 185 LysAspMetHisIleThrTrpTrpLeuIlePheIlePheAlaAsnPheLeuArgGln 204
DB 702 -----TTTAAACTCTCTTAATAATTTCTTTT---TTTGTAGACGG 743
QY 205 SerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLeuGlnPro 224
DB 744 AGTCTGCG-TCGTGTTCAGCTGGAGTGCAGTGGTGCATCTTGAAGCAGCTGTACT 802
QY 225 LeuProProGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAspTrpArg 244
DB 803 CTCATCTCTGGATTCAAGGATTCTCTGCTCAGCTCTGAGTGTGGATTACAGG 862
QY 245 ArgProPro-ArgLeuAlaAsnPhePheValPheLeuValGlu-MetGlyPheThrMetP 264
DB 863 CACCCACCAACAGGCCCCCTAATTTTGTATTTGTAGTAGACAGAGGTTTCACCATGT 922
QY 264 heAlaArgLeuIleLeuSerGlyPro--CysAspLeuProAlaSerAlaSerGlnSe 283
DB 923 TGGACAGGCTGTCTTGAACGGCTGACCTCAGGTGATTCACCCACCCCGGCTCCCAAG 982
QY 283 rAlaGlyIleThrGlyValSerHisHisAlaArgLeuIlePheAsnPheCysLeuPheGln 303

DB 983 TGCTGGGATTACAGCGGTGAGCCACTGCGCCTG-CCCTATTTTATTTTC---TTTTTGA 1038
QY 303 uMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeuGln 323
DB 1039 GATGGAGTCTTGTCTGTGTGCCAGGCTGGAATGAGTGGCGTGTATCTTGGCTCACTGCA 1098
QY 323 nProLeuProProGlyLeuLysArgPhe-SerCysLeuSerLeuProSerSerTrpAspTr 343
DB 1099 ACCCTCTGCTCCAGGTTCAAGTGATTCTTTCAGCCTCAGGCTCCCAAGTAGCTGGATT 1158
QY 343 yrGlyHisLeuProProHisProAlaAsnPheCysIlePheIleArgGlyGlyValSerP 363
DB 1159 ACAGGTGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1218
QY 363 roTyrLeuSerSerGlyTrpSerGlnThrProAspLeu 374
DB 1219 CATGTTGCCAGGCTGGTCTTGAACCTCCTGACCTC 1253
RESULT 11
LOCUS HSM802772/2 2777 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp5471147 (from clone DKFZp5471147).
ACCESSION AL390133
VERSION AL390133.1 GI:9368829
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2777)
AUTHORS Ansong, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M., and
Wiemann, S.
CONSRMT The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp5471147) is available at the RZPD Deutsches
Reisourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp5471147
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
FEATURES
Location/Qualifiers
1..2777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp5471147"
/tissue_type="brain"
/clone_lib="547 (synonym: hfbrl). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="fetal"
/note="genomic"
ORIGIN
Alignment Scores:
Pred. No.: 3.94e-38 Length: 2777
Score: 670.00 Matches: 180
Percent Similarity: 51.17% Conservative: 16
Best Local Similarity: 47.00% Mismatches: 77
Query Match: 32.94% Indels: 111
DB: 3 Gaps: 11
US-09-380-203-2 (1-375) x HSM802772 (1-2777)
QY 1 MetGluPheSerLeuLeuLeuPro---ArgLeuGluCysAsnGlyAlaIleSerAlaHis 19

Db	2764	TTGAGTGGAGTCTCGCTCTGTCGCTCAGCGTGGAGTGCATGGCCCAATCTGGCTCAC	2705
QY	20	ArgAsnLeuArgLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGly	39
Db	2704	CACAGCCTCGGCTCTGGTTTAAAGCGATTCTCTCGCTCAGCCTCCCGAATAGTGGG	2645
QY	40	IleThrGlyMetCysThrHisAlaArgLeuIleLeuTyrPhePheLeuValGluMetGlu	59
Db	2644	ACTATAGGATGTGCCACCGCCAGCTAAATT---TTGTATTATTTTAGTAGACAGGG	2588
QY	60	PheLeuHisValGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSer	79
Db	2587	TTTCACCAITGGCCAGCATGCTCGATCTCTTAACC-----	2549
QY	80	AlaSerGlnSerAlaArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPhe	99
Db	2548	---TTGTGATCGCGCGC-----	2534
QY	100	CysGlyArgAsnArgValSerLeuMetCysProSerTyrSerProGluLeuLysGlnSer	119
Db	2534	-----	2534
QY	120	ThrCysLeuSerLeuProLysCysTyrAspTyrArgAlaAlaValProGlyLeuPhe	139
Db	2533	---CTCAGCCTCCCAAGTGTGGGATTACAG-----	2504
QY	140	IleLeuPhePheLeuArgHisArgCysProThrLeuThrGlnAspGluValGlnTrpCys	159
Db	2504	-----	2504
QY	160	AspHisSerSerLeuGlnProSerThrProGluIleLysHisProProAlaSerAlaSer	179
Db	2503	-----AGTGAGCCACCGTGC-----	2489
QY	180	GlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuIlePheIlePhe	199
Db	2488	---CTGGCCTCTTATTATTATT---CTGGCCTCTTATTATTATT	2468
QY	200	AsnPheLeuArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeu	219
Db	2467	---TTTTTGAGTGGAGTCTCAC-TCTGTGCTCAGGCTGGTGTGCAATGATGCAATCTT	2412
QY	220	GlySerLeuGlnProLeuProGlyPheLysLeuPheSerCysProSerLeuLeuSer	239
Db	2411	GGCTCACTCAGCCTCTGCTCTCAGGTTCAACCAATTCTCTGTCTCAGCCTCTCGAGT	2352
QY	240	SerTrpAspTyrArgArgProPro---ArgLeuAlaAsnPhePheValPheLeuValGlu	258
Db	2351	AGCTGAGATTACAGGATGTGCCATGACCGCTGGCTAATATTTTGGTATTTTAGTAGAG	2292
QY	259	MetGlyPheThrMetPheAlaArgLeuIleLeu---IleSerGlyProCysAspLeuPro	277
Db	2291	ATGGGGTTTCGCCACGTTACCGGGTGTCTCGAACTCTCGCCTCAAGTATTCGCCC	2232
QY	278	AlaSerAlaSerGlnSerAlaGlyIleThrGlyValSerHisHisAla-ArgLeu----	295
Db	2231	GGCTCAGCTCCCAAGTCTGGGATTACAGCATGAGCCACACACCTGGCCTTTTCT	2172
QY	296	---IlePheAsnPheCysLeuPheGluMetGluSerHisSerValThrGlnAlaGlyVa	314
Db	2171	TTTTCTAATTATTTATTTATTTAAATGGAGTCTCGCTCTGTGGCCAGTTGATGT	2112
QY	314	IleTrpProAsnLeuGlySer---LeuGlnProLeuProProGlyLeuLysArgPheSe	333
Db	2111	GCAGTGGCGCAATCTTTGGCTCACCACCGCTCTCTCTCCAGGTTCCAGTGATTC	2052
QY	333	rCysLeuSerLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPh	353
Db	2051	GTGGCTCAGCCTCCCAAGTAGTGGGACTACAGGATGTGCCACACACCCAGCTAATTT	1992
QY	353	eCysIlePheIleArgGlyGlyValSerProTyrLeuSerGlyTyrTrpSerGlnThrProAs	373

Db	1991	TTGTATTATTTTAGTAGACAGGGTTTAAACCATTTTGACCACCGCTGGTCTTGAACTCCTGA	1932
QY	373	pleuArg 375	
Db	1931	CCTCAAG 1925	
RESULT 12			
BC032537		3021 bp	mRNA
LOCUS			
DEFINITION			Homo sapiens hypothetical protein LOC63929, mRNA (cDNA clone IMAGE:5527890), with apparent retained intron.
ACCESSION			BC032537
VERSION			BC032537.1
KEYWORDS			HTC.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			1 (bases 1 to 3021)
AUTHORS			Strausberg,R.D., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uscin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fanev,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE			Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE			22388257
PUBMED			12477932
REFERENCE			2 (bases 1 to 3021)
AUTHORS			Strausberg,R.
TITLE			Direct Submission
JOURNAL			Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK			NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT			Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTDP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nihri.nih.gov Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.J., McCliskey,J.C., McDowell,J., Pearson,R., Stantiripop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 69 Row: i Column: 17
 This clone was selected for full length sequencing because it

passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: retained intron.

FEATURES

source

Location/Qualifiers
1. 3021
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5527890"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.: 1 67e-37 Length: 3021
Score: 662.00 Matches: 174
Percent Similarity: 53.56% Conservative: 29
Best Local Similarity: 45.91% Mismatches: 87
Query Match: 32.55% Indels: 91
DB: Gaps: 11

US-09-380-203-2 (1-375) x BC032537 (1-3021)

QY 10 LeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeuProGlySerSerAsp 29
Db 369 ATGGAGTGCAGTGGCGTATCTCAGCTCACTACAACTCGCCATCGGTTGGGCAAT 428
QY 30 SerProAlaSerAlaSerProValAlaGlyIleThrGlyMetCysThrHisAlaArgLeu 49
Db 429 TCTCTGCTCGCTCCGCTCCGGGTAGTGGGACTACAGGTGCAGCTGCCATGCCAGCTA 488
QY 50 IleLeuTyrPhePheLeuValGluMetGluPheLeuHisValGlyGlnAlaGlyLeuGlu 69
Db 489 ATT---TTTGTATTATTAGAGACGGGGTTTACCCTGTGTCAGGCGCGCTCTCAA- 544
QY 70 LeuProThrSerAspProSerValSerAlaSerGlnSerAlaArgTyrArgThrGly 89
Db 544 ----- 544
QY 90 HisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAsnArgValSerLeuMetCys 109
Db 544 ----- 544
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QY 130 TyrArgArgAlaAlaValProGlyLeuPheIleLeuPhePheLeuArgHisArgCysPr 149
Db 596 TACAGCGGTGAGCCACTGACCCAGCGCTTTTAAAGTTTAAATGACATATAATGTAC 655
QY 149 oThrLeuThrGlnAspGluValGlnTrp-----CysAspHisSerSerLeuGlnPr 166
Db 656 GTATTATA-----CAGGTAATAATGATGTTTGATACATATAATGAT 700
QY 166 oSerThrProGluIleLysHisProProAlaSerAlaSerGlnValAlaGlyThrLysAs 186
Db 701 CAGATCAGAACAAATTAGCATATCCA----- 725
QY 186 pMetHisHisTyrThrTrpLeuIlePheIle-----PheIlePheAsnPheLe 202
Db 726 -----TCACATGACATATTATCATTTATTGTGTGAGCTTTAGTTCTTTTTTTTTT 781
QY 202 uArgGlnSerLeuAsnSerValThrGlnAlaGlyValGlnTrpArgAsnLeuGlySerLe 222
Db 782 GGGATAGAGTCTCAC-TCTGTCAACCGGCTGGAGTACAGTGTGTGATCTTTGGCTCACT 840
QY 222 uGlnProLeuProProGlyPheLysLeuPheSerCysProSerLeuLeuSerSerTrpAs 242
Db 841 GCAACCTCCACCCACCGGCTTCGACCAATTCTCTGCTCCAGCTCCCTAGTAGTGGGA 900

QY 242 pTyrArgArg-----ProProArgLeuAlaAsnPhePheValPheLeuValGluMetGlyPh 261
Db 901 TTACAGGACACCTGCCACACAC-----CCATTTTGTATTATTTTAGTAGACCGGGTT 954
QY 261 eThrMetPhe-----AlaArgLeuIleLeuSerGlyProCysAspLeuProAlaSe 279
Db 955 TCACCATCTTGGCCAGGCGAGCTGCTGTGATCTCTGACCTTGTGATCCACCCACCTC 1014
QY 279 rAlaSerGlnSerAlaGlyIleThrGlyValSerHisAlaAlaArgLeuIlePheAsnPh 299
Db 1015 GGCCTCCCAAACTGCTGGATTACAGGATGAGGCGGCGGCGG----- 1057
QY 299 eCysLeuPheGluMetGluSerHisSerVal-----ThrGlnAlaGlyValGlnTr 316
Db 1058 -----CAGCCAGACAGACAGTCTTGTCTTGTCCAGGCTGGAGTGTAGTG 1101
QY 316 pProAsnLeuGlySerLeuGlnProLeuProGlyLeuLysArgPheSerCysLeuSe 336
Db 1102 GCGCCATCTTGGCTCACTGCAACCTCCAACTCCCTGGTTCAAGCAGATTCTCTGCTCAG 1161
QY 336 rLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIlePh 356
Db 1162 CTTCCCAAGTAGCTGGATTACAGCAGCAGCAGCAGCAGTAAATTTTGTATT 1221
QY 356 eIleArgGlyGlyValSerProTyrLeuSerGlyTrpSerGlnThrProAspLeu 374
Db 1222 TAGTAGACAGAGGTTTCCACCATGTGGCCAGGATGGTCTTGTATCTCTGACCTC 1276

RESULT 13

BC047576

LOCUS

DEFINITION

BC047576 2874 bp mRNA linear HTC 19-NOV-2003

Homo sapiens hypothetical protein FLJ20542, mRNA (cDNA clone

IMAGE:4814349), containing frame-shift errors.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 2874)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Brange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shenvchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2874)
Strausberg, R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk

REMARK

COMMENT

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 90 Row: d Column: 9
 This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
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 /note="Vector: pBluescript"

ORIGIN

Alignment Scores:

Pred. No.: 3 63e-37 Length: 2874
 Score: 657.00 Matches: 191
 Percent Similarity: 54.16% Conservatives: 24
 Best Local Similarity: 48.11% Mismatches: 103
 Query Match: 32.30% Indels: 82
 DB: 3 Gaps: 10

US-09-380-203-2 (1-375) x BC047576 (1-2874)

QY 4 SerLeuLeuLeuProArgLeuGluCysAenGlyAlaIleSerAlaHis-ArgAsnLeuAr 23
 DB 67 TGGCTCTCATGCGCGGCTAGTGCAGTGGTGGGATCTCGGCTCACCTTGAACCTCG 126
 QY 23 gLeuProGlySerSerAspSerProAlaSerAlaSerProValAlaGlyIleThrGlyWe 43
 DB 127 CTTCTGGGTTCAAGCGATTCCTGCTCGGCTCCCGAGTAGCTGGGATACAGGCGT 186
 QY 43 tCystHisAlaArgLeuLeuLeuTyrPhePheLeuValGluMetGluPheLeuHisVa 63
 DB 187 GTGCCACCACACCCAGTTAATTTTGTATTTTATTTAGTAGAGACGGGGTTTACCGTGT 246
 QY 63 lGlyGlnAlaGlyLeuGluLeuProThrSerAspAspProSerValSerAlaSerGlnSe 83
 DB 247 TGGTCAGGCTGCTTGAAC----- 267
 QY 83 xAlaArgTyrArThrGlyHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAs 103
 DB 267 ----- 267
 QY 103 nArgValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSe 123
 DB 268 -----CCTGATCTCAGGTGATCCACCGCGCTGG 296
 QY 123 rLeuProLysCysTrpAspTyrArgArg--AlaAlaValProGlyLeuPheIleLeuPhe 142
 DB 297 TCTCCAGAGTGTGGGATTGAGGAGTAGGACCACTGCGCTCGGCCCAAAATTTTGTGTTT 356
 QY 143 PheLeuArgHisArg-----CysProThrLeuThrGlnAspGluVal 156
 DB 357 AAATGGCTGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 416
 QY 157 GlnTrpCysAspHisSerSerLeuGlnProSerThrProGluLeuIleLysHisProAla 176
 DB 417 GAG-----GCGGGAGGACGCTTGAGCCCGCAGGAGTT---TGAGTGAGCCATGATTCGCC 467

QY 177 SerAlaSerGlnValAlaGlyThrLysAspMetHisHisTyrThrTrpLeuLeuPheIle 196
 DB 468 ACTGAGCGCTGGGTGACAGCCCA-----CCCTGTCTCTCAATTTT 509
 QY 197 PheIlePheAenPheLeuArgGlnSerLeuAenSerValThrGlnAlaGlyValGlnTrp 216
 DB 510 TTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 568
 QY 217 ArgAsnLeuGlySerLeuGlnProLeuProGlyPheLeuLysLeuPheSerCysProSer 236
 DB 569 CGCGATCTCGGCTTACTGCAACCTCCGCTCCCGGTTCCGAGCAGTCTCTCCGCTCCAGC 628
 QY 237 LeuLeuSerSerTrpAspTyr---ArgArgProProArgLeuAlaAsnPhePheValPhe 255
 DB 629 CTCGAGTAGTGGGATTGGCGGCGCGCCACACACATCCGCGCTAAT---TTTGTATTT 685
 QY 256 LeuValGluMetGly-PheThrMetPheAlaArgLeuLeuLeuSerGlyPro--Cys 274
 DB 686 TTAGTGGAGACGGGCTTTTTCGTTGGTTCAGGCTGGTCTTGAATTTCCCAACCTCAGGT 745
 QY 275 AspLeuProAlaSerAlaSerGlnSerAlaGlyIleThrGlyValSerHisAlaArg 294
 DB 746 GATCCACCGCTCAGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGCACC 805
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 DB 806 CAAAGTTTAAATGAATAAATTTAAAGAGAGCTAGTTTTTTTGCCAAATTTTGT 865
 QY 303 GluMetGluSerHisSerValThrGlnAlaGlyValGlnTrpProAsnLeuGlySerLeu 322
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 DB 982 TGCAGGCGCCACCCACCATGCCAGCTAACTTTTGTGTTTGTAGTGGAGACAGGGTTTCA 1041
 QY 363 ProTyrLeuSerGlyTrpSerGlnThrProAspLeuArg 375
 DB 1042 CCGTCTCGCGGAGTGTCTTGAACCTCTGACTTCAGA 1080
 RESULT 14
 AW600804/c
 LOCUS
 DEFINITION
 N26-20 Human leukocyte MATCHMAKER cDNA Library Homo sapiens cdna,
 mRNA sequence.
 ACCESSION
 VERSION
 AW600804.1 GI:7304735
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 990)
 AUTHORS
 Meng, X., Song, Y., Mao, J. and Sun, Z.
 TITILE
 Proteins that interact with NBS
 JOURNAL
 Chin. J. Radiol. Med. Prot. (2000) In press
 COMMENT
 Contact: Meng X
 Department of Biochemistry and Molecular Biology
 Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing, 100850, P.R. China
 Tel: 861068214653
 Fax: 861068214653
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 Location/Qualifiers
 1..990
 /organism="Homo sapiens"
 /mol_type="mRNA"
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QY	259	MetGlyPheThrMetPheAlaArgLeuLeuLeuLeuSerGlyProCysAspLeuProAla	278
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QY	279	SerAlaSerGlnSerAlaGlyLeuThrGlyValSerHisAlaArgLeuLeuPheAsn	298
DB	257	TACAGCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCTATTATTT	198
QY	299	PheCysLeuPhe-----GluMetGlnSerHisSerValThrGlnAlaGlyValGln	315
DB	197	TTTAAATTTTATTTTGTGTGAGACAGAGTCTAGCTCTATCTGTCAGGCTGGAGTCCAG	138
QY	316	TTPProAsnLeuGlySerLeuGlnProLeuProGlyLeuLeuLeuPheSerCysLeu	335
DB	137	TGGTGTGATCTCAGCCCACTCAACCTCCGCTCCCGGGTTCAAGATGATTCTCTCGCTC	78
QY	336	SerLeuProSerSerTrpAspTyrGlyHisLeuProProHisProAlaAsnPheCysIle	355
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QY	356	PheIle 357	
DB	17	TTTGTCT 12	
RESULT	15		
LOCUS	CR627381	3775 bp mRNA linear HTC 22-SEP-2000	
DEFINITION		Homo sapiens mRNA; cDNA DKFzp762F237 (from clone DKFzp762F237).	
ACCESSION	CR627381		
VERSION	CR627381.1	GI:50949857	
KEYWORDS		HTC.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		1 (bases 1 to 3775)	
		Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,	
		Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and	
		Wiemann,S.	
CONSTRM		The German cDNA Consortium	
TITLE		Direct Submission	
JOURNAL		Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764	
COMMENT		Neuherberg, GERMANY	
		Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
		Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; the	
		sequencing consortium of the German Genome Project.	
		This clone (DKFzp762F237) is available at the RZPD Deutsches	
		Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.	
		Please contact RZPD for ordering.	
		http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFzp762F237	
		Further information about the clone and the sequencing project is	
		available at http://mips.gsf.de/projects/cdna/.	
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		/tissue type="melanoma (MeWo cell line)"	
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		DH10B; sites NotI + SalI"	
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		/db_xref="GI:50949858"	

